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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 119 Seconds

(without alignments)

34.425 Million cell updates/sec

Title: US-10-036-918B-4**Perfect score:** 33**Sequence:** 1 XPKRRLXL 8**Scoring table:** BLOSUM2**Gapext 10.0 , Gapext 0.5****Searched:**

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378**Minimum DB seq length:** 0
Maximum DB seq length: 200000000**Post-processing:** Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries**Database :** UniProt_03;*
1: uniprot_sprot;*
2: uniprot_trembl;***Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	269	2	07NFR5
2	30	90.9	285	2	096W33
3	30	90.9	295	2	P95666
4	30	90.9	320	2	Q98K74
5	30	90.9	325	2	Q8EH66
6	30	90.9	333	2	Q89ML3
7	30	90.9	360	2	Q8UH95
8	30	90.9	460	1	Q7JPK1
9	30	90.9	540	1	Q7V8Q2
10	30	90.9	569	2	Q52305
11	30	90.9	877	1	Q23853
12	30	90.9	1100	1	JAK3_RAT
13	29	87.9	157	2	Q96WZ4
14	29	87.9	253	2	Q30393
15	29	87.9	257	2	Q7PB33
16	29	87.9	312	2	Q9PI62
17	29	87.9	313	2	Q8RG99
18	29	87.9	315	1	ACCA_HAEIN
19	29	87.9	315	2	Q886W7
20	29	87.9	315	2	Q88G4
21	29	87.9	316	2	Q88BQ8
22	29	87.9	316	2	Q9HXZ2
23	29	87.9	317	2	Q7VP13
24	29	87.9	317	2	Q7D2H6
25	29	87.9	317	2	Q9Cnx9
26	29	87.9	318	1	ACCA_ECOLI
27	29	87.9	318	1	ACCA_SALTY
28	29	87.9	319	2	Q667k5
29	29	87.9	319	2	Q8PAW9
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ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
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29	29	87.9	319	2	Q8PAW9
30	29	87.9	319	2	Q8PMM1
31	29	87.9	319	2	Q8ZHS2

RESULT 1		Best Local Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
ID	Q7NFB5	PRELIMINARY;	PRT;	269 AA.	Qy	2 PXRPyXL 8	Ox
AC	Q7NFB5;				Db	21 PSRPyTL 27	
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)						
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)						
DE	GJ13641 protein.						
GN	OrderedlocusName=gJ13641;						
OC	Gloebacter violaceus.						
OX	Bacteria; Cyanobacteria; Chroococcales; Gloebacter.						
RA	NCBI_TAXID=33072;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	SPRAIN=PCC 7421;						
RX	MEDLINE=22977040; PubMed=14621292;						
RA	Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T., Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyohara C., Kohara M., Matsumoto A., Nakazaki N., Shimpou S., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of <i>Gloebacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids.";						
RT	DNA Res. 10;137:145 (2003).						
RL	EMBL; AP00580; BAC91582.1; -;						
KW	Complete proteome.						
SQ	SEQUENCE 269 AA; 30697 MW; 67644AFBA107FF2B CRC64;						
Query Match	90.9%; Score 30; DB 2; Length 269;						
Best Local Similarity	71.4%; Pred. No. 2.3e+02;						
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
Qy	2 PXRPyXL 8						
Db	186 PARPyTL 192						
RESULT 2		Best Local Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Q96WP3	PRELIMINARY;	PRT;	286 AA.	Qy	2 PXRPyXL 8	Ox	
ID	Q96WP3			Db	21 PSRPyTL 27		
AC	Q96WP3;						
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)						
DT	01-DEC-2004 (TREMBLrel. 26, Last annotation update)						
DE	Urease.						
GN	Name=URE;						
OS	Arthroderra benhamiae (Trichophyton mentagrophytes)						
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;						
OC	Oxygenales; Arthrodertaceae; Arthroderra.						
OX	NCBI_TAXID=63400;						
RN	{1}						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=VUT-77011;						
RC	Kano R., Hasegawa A.; Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.						
RL	- CATALYTIC ACTIVITY: Urea + H ₂ O = CO(2) + 2 NH(3)						
CC	-- COFACTOR: Binds 2 nickel ions per subunit (By similarity).						
CC	-- SIMILARITY: Belongs to the urease family.						
DR	EMBL; AB069970; BAB62910.1; -.						
DR	HSSP; P18314; IEJK.						
DR	InterPro; IPRO05848; Urease alpha.						
DR	InterPro; IPRO05848; Urease alpha.						
DR	Pfam; PF01979; Amidohydro_1; 1.						
DR	PRINTS; PR01752; UREASE						
DR	PROSITE; PS00145; UREASE 2; 1.						
KW	Hydrolase; Metal-binding; Nickel.						
SQ	SEQUENCE 286 AA; 31471 MW; ADD90EA7BCB9A7 CRC64;						
Query Match	90.9%; Score 30; DB 2; Length 286;						

		DR	PR00165; HTH ARAC; 2.
		DR	PRINTS; PR00032; HTARAC.
		DR	SMART; SM0042; HTH ARAC; 1.
		DR	PROSITE; PS0124; HTH ARAC_FAMILY_2; 1.
KW	Complete proteome; DNA-binding; Transcription;		
SQ	SEQUENCE 320 AA; 35277 MW; 0A2C56DBD6C3ED2B CRC4;	RESULT 5	
OY	2 PXRPyXL 8	PRT;	325 AA.
Db	32 PARPYAL 38	PRT;	333 AA.
RN	[1]	PRT;	333 AA.
O8EH65	PRELIMINARY;	PRT;	325 AA.
ID	O8EH66	PRT;	325 AA.
AC	O8EH66;	PRT;	325 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Created)	PRT;	325 AA.
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	PRT;	325 AA.
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	PRT;	325 AA.
DB	Iron-sulfur cluster-binding protein.	PRT;	325 AA.
GN	OrderedlocusName=SO0364;	PRT;	325 AA.
OS	Shewanellaceae; Shewanella.	PRT;	325 AA.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;	PRT;	325 AA.
OX	NCBI_TaxID=70863;	PRT;	325 AA.
RN	[1]	PRT;	325 AA.
RP	SEQUENCE FROM N.A.	PRT;	325 AA.
RC	STRAIN=MR-1;	PRT;	325 AA.
RX	MEDLINE=22297686; PubMed=1236813; DOI=10.1038/nbt749;	PRT;	325 AA.
RA	Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,	PRT;	325 AA.
RA	Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,	PRT;	325 AA.
RA	Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,	PRT;	325 AA.
RA	Brinkac L.M., Daugherty S.C., Debey R.T., Dodson R.J., Burkin A.S.,	PRT;	325 AA.
RA	Raff D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,	PRT;	325 AA.
RA	White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,	PRT;	325 AA.
RA	Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,	PRT;	325 AA.
RA	Uitterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,	PRT;	325 AA.
RA	Venter J.C., Nealson K.H., Fraser C.M.,	PRT;	325 AA.
RT	Genome sequence of the dissimilatory metal ion-reducing bacterium	PRT;	325 AA.
RT	Shewanella oneidensis.	PRT;	325 AA.
RL	Nat. Biotechnol. 20:1118-1123 (2002).	PRT;	325 AA.
DR	EMBL; AE015580; RAN54429.1; -.	PRT;	325 AA.
DR	RRSP; P02426; 4PSC.	PRT;	325 AA.
DR	TIGR; S01364; -.	PRT;	325 AA.
DR	GO; GO:0005489; F:electron transporter activity; IEA.	PRT;	325 AA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	PRT;	325 AA.
DR	InterPro; IPR006058; 2rezs_fd_BS.	PRT;	325 AA.
DR	InterPro; IPR001834; Cyt_B5_reductase.	PRT;	325 AA.
DR	InterPro; IPR008333; FAD_binding_6.	PRT;	325 AA.
DR	InterPro; IPR001041; Ferrredoxin.	PRT;	325 AA.
DR	InterPro; IPR001709; FPN_cyt_reductse.	PRT;	325 AA.
DR	InterPro; IPR001433; Oxrd_FAD/NAD(P).	PRT;	325 AA.
DR	PFam; PF00970; FAD_binding_6; 1.	PRT;	325 AA.
DR	PFam; PF00111; Fad2; 1.	PRT;	325 AA.
DR	PFam; PF00175; NAD binding_1; 1.	PRT;	325 AA.
DR	PRINTS; PR00406; CYTBSDTASE.	PRT;	325 AA.
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN_1.	PRT;	325 AA.
DR	PRE2S; Complete proteome; Iron-sulfur; Metal-binding.	PRT;	325 AA.
KW	SEQUENCE 325 AA; 3526 MW; EA7CA80771C738E CRC64;	PRT;	325 AA.
Query Match	90.9%; Score 30; DB 2; Length 325;	RESULT 6	
Best Local Similarity	71.4%; Pred. No. 2.8e+02;	PRT;	360 AA.
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	PRT;	360 AA.
OY	2 PXRPyXL 8	PRT;	360 AA.
Db	45 PARPYAL 51	PRT;	360 AA.
RN	[1]	PRT;	360 AA.
O8HMF5	PRELIMINARY;	PRT;	360 AA.
ID	O8HMF5	PRT;	360 AA.
AC	O8HMF5; Q7D099;	PRT;	360 AA.
DT	01-JUN-2002 (TREMBLrel. 21, Created)	PRT;	360 AA.
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)	PRT;	360 AA.
DE	Ferrredoxin_I (AGR_C_3321p).	PRT;	360 AA.
GN	OrderedlocusName=AGR_C_1321; Atu0727;	PRT;	360 AA.
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).	PRT;	360 AA.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;	PRT;	360 AA.
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium;	PRT;	360 AA.
OX	NCBI_TaxID=176299;	PRT;	360 AA.
RA	SEQUENCE FROM N.A.	PRT;	360 AA.
RC	STRAIN=Dupont;	PRT;	360 AA.
RX	MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;	PRT;	360 AA.
RA	Wood D.W., Setubal J.C., Kaul R., Monk D.E., Kitajima J.P.,	PRT;	360 AA.
RA	Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L.,	PRT;	360 AA.
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. S., Chapman P., Cleland J., Deatherage G., Gillett W., Grant C.,	PRT;	360 AA.
RA	Kutyaev T., Levy R., Li M.-J., McClelland E., Palmeri A.,	PRT;	360 AA.

RA Raymond C., Rouse G., Saengphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespen W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrickson C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 CS8.",
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SOURCE FROM N.A.
 RC STRAIN_Cereor;
 RX MEDLINE=2168851; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
 RA Qurollo B., Goldman B.S., Cao Y., Askew M., Halling C., Mullin L.,
 RA Rounik J., Gordon J.J., Vaudin M., Tarchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Marieb B.,
 RA Flanagan C., Crowell C., Gibson J., Lomo C., Gear C., Strub G.,
 RA Cielo C., Slatter S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens CS8.",
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009041; AAL41743.1; -.
 DR EMBL; AE008007; ARK86537.1; -.
 DR PIR; H97447; H97447.
 DR IESB; P00216; IEB02.
 DR GO; GO:000589; Fe-electron transporter activity; IEA.
 DR GO; GO:0016491; Fe-oxidoreductase activity; IEA.
 DR GO; GO:0006118; Fe-electron transport; IEA.
 DR InterPro; IPR006058; 2re2S fd_BS.
 DR InterPro; IPR00833; FAD_binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FDN_cyt_reductse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR InterPro; IPR001221; Phe_hydroxylase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; Fez2; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00071; FPNCR.
 DR PRINTS; PR00010; PHENYRLXASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN_1; Metal-binding; Complete_proteome.
 KW 2FE2S; Iron; Iron-sulfur; Metal-binding; Complete_proteome.
 SQ SEQUENCE 360 AA; 39804 MW; 4EEFF7493E850BA0 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRXXL 8
 Db 77 PSRBYAL 83

RESULT 8

QJPK1 PRELIMINARY; PRT; 460 AA.

ID QJPK1; PRELIMINARY; PRT; 460 AA.

AC QJPK1; PRELIMINARY; PRT; 460 AA.

DT 05-JUL-2004 (Tremblel, 27, Created)
 DT 05-JUL-2004 (Tremblel, 27, Last sequence update)
 DT 05-JUL-2004 (Tremblel, 27, Last annotation update)

DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxId=4689;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN_A3;
 RX MEDLINE=91002566; PubMed=1976383;
 RA Giorda R., Ohmachi T., Shaw H.L., Ennis H.L.,
 RT "A shared internal threonine-glutamic acid-threonine-proline repeat
 defines a family of Dictyostelium discoideum spore germination
 specific proteins";
 RL Biochemistry 29:7264-7269 (1990).

RN [2]
 RP SOURCE FROM N.A.
 RC STRAIN_A3;
 RA Giorda R., Ohmachi T., Shaw H.D.R., Ennis H.L.;
 RA Submitted (FEB-1995) to the EMBL/GenBank/DDJB databases.
 RL EMBL; U20661; ARB54078.1; -.
 DR InterPro; IPR008999; Actin_crosslink.
 KW Hypothetical protein.

SEQUENCE 460 AA; 51264 MW; 799492509ACCC66F6 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 460;
 Best Local Similarity 71.4%; Pred. No. 4.2e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRXXL 8
 Db 72 PSPPYTL 78

RESULT 9

SYN_SINTO SYN_SINTO STANDARD; PRT; 540 AA.

ID SYN_SINTO STANDARD; PRT; 540 AA.

AC Q971D8; -.

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS).
 DE Name=pheS; OrderdLocusNames=STI415;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=11955;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN_JCM 10545 / ?;
 RX MEDLINE=21456156; PubMed=11574749;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankei A., Kosugi H., Horoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Osuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshihara T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 Crenarchaeon, Sulfolobus tokodaii strain7";
 RL DNA Res. 8:123-140 (2001)
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA (Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA (Phe).
 CC -1- SUBUNIT: Trimer of two alpha and two beta chains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain
 family. Subfamily 2.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 EMBL; AF000586; BAB66482.1; -.
 DR InterPro; IPR005147; B5.
 DR InterPro; IPR004531; PheT_arch.
 DR InterPro; IPR00961; Putativ_DNA_bind.
 DR Pfam; PF03483; BS_4; 1.
 DR Pfam; PF03484; BS_1; 1.
 DR TIGRFAMS; TIGR00471; PheT_arch; 1.
 KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;

KW PROTEIN BIOSYNTHESIS; 540 AA; 61519 MW; 9E6A5EB4A923E43 CRC64;

SQ [1] SEQUENCE FROM N.A.

Query Match 90.9%; Score 30; DB 1; Length 540;
Best Local Similarity 71.4%; Pred. No. 5+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRRLXL 8

Db 90 PSRPYAL 96

RESULT 10

ID 052305 PRELIMINARY; PRT; 569 AA.

AC 052305; STRAIN=x3; PRT; 569 AA.

DT 01-JUN-1998 (TREMBLel. 06, Created)
01-MAR-2004 (TREMBLel. 26, Last sequence update)

RT Urea alpha subunit.

DR Name=ureC;

OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.

OX NCBI_TaxID=33049;

RN [1]

RP STRAIN=PCC_7002;

RX MEDLINE=98330571; PubMed=9647800;

RA Sakamoto T., Delgizzo V.B.; Bryant D.A.;
Appl. Environ. Microbiol. 66:2361-2366(1998). "

RT "Growth on urea can trigger death and peroxidation of the cyanobacterium Synechococcus sp. strain PCC 7002.";

RL CCA -I - CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3)

CC -I - COFACTOR: Binds 2 nickel ions per subunit (By similarity).

CC -I - SIMILARITY: Belongs to the urease family.

DR EMBL; AP035751; AAC26155.1; -.

DR HSPB; P18314; 1EJX.

DR GO; GO:0016787; Hydrolase activity; IEA.

DR GO; GO:001651; F:nickel ion binding; IEA.

DR GO; GO:0009039; F:urease activity; IEA.

DR GO; GO:0006807; F:nitrogen metabolism; IEA.

DR InterPro; IPR006680; Amidohydrolase.

DR InterPro; IPR011059; Metalo hydrolase.

DR InterPro; IPR053848; Urease_alpha.

DR InterPro; IPR008215; Urease_alpha_lone.

DR PFAM; PF01979; Amidohydro_1; 1.

DR PRINTS; PIRSF001226; Urease_alpha; 1.

DR PRINTS; PIRSF001225; Urease_alpha; 1.

DR TIGRFAM; TIGR01792; urease_alpha; 1.

DR PROSITE; PS00145; UREASE_1; 1.

DR Hidrolase; Metal-binding; Nickel.

SQ SEQUENCE 569 AA; 61820 MW; DB717CA5B1642A93 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 569;
Best Local Similarity 71.4%; Pred. No. 5.3+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRRLXL 8

Db 302 PTRPYTL 308

RESULT 11

ID Q23853 PRELIMINARY; PRT; 877 AA.

AC Q23853; STRAIN=x3; PRT; 877 AA.

DT 01-NOV-1996 (TREMBLel. 01, Created)
01-NOV-1998 (TREMBLel. 08, Last sequence update)

DT 01-MAR-2004 (TREMBLel. 26, Last annotation update)

RT Hypothetical protein (Fragment).

DB Dictyostelium discoideum (Slime mold).

OS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

RN [1]

NCBI_TaxID=44689;

RN SEQUENCE FROM N.A.

RT Submitted (FEB-1995) to the EMBL/Genbank/DDJB databases.

DR EMBL; U0061; AAC54079.1; -.

DR DICTYBASE; DDB018705; gers.

DR GO; GO:000524; F:ATP binding; IEA.

DR GO; GO:0004672; F:protein kinase activity; IEA.

DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

DR InterPro; IPR01009; Kinase_like.

KW HYPOTHETICAL PROTEIN.

FT NON_TER 1

SQ SEQUENCE 877 AA; 98709 MW; ECDB726FB1CA66CB CRC64;

Query Match 90.9%; Score 30; DB 2; Length 877;
Best Local Similarity 71.4%; Pred. No. 8.6e+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRRLXL 8

Db 489 PSRPYTL 495

RESULT 12

ID JAK3 RAT STANDARD; PRT; 1100 AA.

AC Q63272; STRAIN=x3; PRT; 1100 AA.

DT 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tyrosine-protein kinase JAK3 (EC 2.7.1.112) (Janus kinase 3) (JAK-3).

GN Name=Jak3;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP STRAIN FROM N.A.

RC TISSUE-Spleen;

RX MEDLINE=9412816; PubMed=8143863; DOI=10.1016/0014-5793(94)80485-0;

RA Takahashi T., Shirasawa T.; J. Biol. Chem. 270:1823-1829 (1995).

RT "Molecular cloning of rat JAK3, a novel member of the JAK family of protein tyrosine kinases.";

RL FERS Lett. 342:124-128 (1994).

-I - FUNCTION: Tyrosine kinase of the non-receptor type, involved in the interleukin-2 and interleukin-4 signaling pathway.

CC -I - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -I - SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane associated (By similarity).

CC -I - FUNCTION: Tyrosine phosphorylated in response to IL-2 and IL-4 (By similarity).

CC -I - SIMILARITY: Belongs to the Tyr protein kinase family. JAK subfamily.

CC -I - SIMILARITY: Contains 1 FERM domain.

-1- SIMILARITY: Contains 1 SH2 domain.

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CC EMBL; D28508; BA005868.1; -.

CC PIR; S43677; S43677.

DR HSSP; P11362; 1FGK.

DR RGD; 2940; Jak3.

DR InterPro; IPR000599; Band_4.1.

DR InterPro; IPR009127; JAK.

DR InterPro; IPR009130; JAK3.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; prot_kinase.

DR InterPro; IPR003880; SH2.

DR InterPro; IPR001445; Tyr_pk kinase.

DR InterPro; IPR008266; Tyr_pk kinase_AS.

DR Pfam; PF0069; Pkinase_2.

DR Prints; PR01823; JANUSKINASE.

DR Prints; PR01026; JANUSKINASE3.

DR Prints; PR00105; TYRKINASE.

DR Prints; PD000001; FERM_1; FALSE_NEG.

DR Prints; PS0057; FERM_3; 1.

DR SMART; SMO295; B41; 1.

DR SMART; SMO295; SH2; 1.

DR SMART; SMO252; SH2; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00661; FERM_2; FALSE_NEG.

DR PROSITE; PS0057; FERM_3; 1.

DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.

DR PROSITE; PS50001; SH2; FALSE_NEG.

KW ATP-binding; Phosphorylation; Repeat; SH2 domain; Transferase; Tyrosine-protein kinase.

FT DOMAIN 24 353 FERM.

FT DOMAIN 372 472 SH2 (atypical).

FT DOMAIN 517 777 Protein kinase 1.

FT DOMAIN 818 1091 Protein kinase 2.

FT NIP BIND 824 832 ATP (By similarity).

FT BINDING 851 851 Proton acceptor (By similarity).

FT ACT SITE 945 976 Phosphotyrosine (by autocatalysis) (By similarity).

FT MOD_RES 976 976 Kawabata A., Hikiji T., Kobatake N., Inada K., Ikeda Y., Ohmoto S., Okutani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Konatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kuchi H., Masuno Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Suano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs"; Nat. Genet. 36:40-45 (2004). [2]

RN 1100 AA; 122560 MW; 1D59CA05FADD7E2 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 1100; Best local Similarity 71.4%; Pred. No. 1.1e+03; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPyXL 8
Db 228 PSRPYAL 234

RESULT 13

Q6MZA4 PRELIMINARY; PRT; 157 AA.

AC Q96M24; DT 01-DEC-2001 (TREMBREL_19_Created)
DT 01-DEC-2001 (TREMBREL_19_Last sequence update)

DE 25-OCT-2004 (TREMBREL_28_Last annotation update)

DE Hypothetical protein FLJ31659;
Name=FLJ31659;

OS Homo sapiens (Human);
Ox Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo. NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PUBMED=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Ottuki T., Sugiyana T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makira H., Seike M., Obayashi M., Nishi T., Shiba T., Yamamoto J., Saito K., Kawai Y., Isomo Y., Nakamura Y., Naganari K., Yamamoto K., Yesuda T., Iwayangi T., Wagatsuma M., Shiratori A., Murakami K., Seno T., Kondo H., Sugawara M., Sudo H., Hoboiri T., Kaku Y., Kodaira H., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Niromiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kinata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe M., Hotuta T., Kubano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiva S., Komai F., Hara R., Takeuchi K., Aritta M., Imose N., Musashino K., Yuki H., Oshima A., Sasaki N., Notsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiono T., Mori Y., Momiyama H., Satoh N., Tamai S., Terashima Y., Suzuki O., Nakagawa S., Seno A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Wakanae T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Takashio H., Tanigami A., Fujivara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inada K., Ikeda Y., Ohmoto S., Okutani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Konatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kuchi H., Masuno Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Suano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs"; Nat. Genet. 36:40-45 (2004). [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RC MEDLINE=2338257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner D., Schenner C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Sores M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Manly D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton M., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J.J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilus D.E., Schenck A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RC Strausberg R.L., Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK056221; BAB71123.1; -.

KW Hypothetical Protein.

SQ SEQUENCE 157 AA; 17021 MW; TDAGA84FF963BDF56 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 157; Best local Similarity 71.4%; Pred. No. 2e-02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPyXL 8

DB	43	PNRPTI 49
RESULT	14	
003093	PRELIMINARY;	PRT; 253 AA.
ID	Q03093	
AC	Q3093;	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Thioesterase;	
OS	Streptomyces hygroscopicus.	
OC	Bacteria; Actinobacteria; Actinomycetales;	
OC	Streptomycineae; Streptomycetaceae; Streptomyces.	
OX	NCBI_TaxID=1912;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE-91294191; PubMed=2066341;	
RA	RaiBaud A., Zalacain M., Holt T.G., Tizard R., Thompson C.J.;	
RT	"Nucleotide sequence analysis reveals linked N-acetyl hydrolase', thioesterase, transport, and regulatory genes encoded by the bialaphos biosynthetic gene cluster of Streptomyces hygroscopicus.";	
RL	J. Bacteriol. 173:4454-4463(1991).	
DR	EMBL; Me4783; AAA:9278.1; -.	
DR	PRR; C47031; C47031.	
DR	GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.	
DR	GO; GO:0009058; P:biogenesis; IEA.	
SQ	SEQUENCE 253 AA; 27630 MW; 26602C0D0EBC2A3 CRC64;	
Query Match	87.9%; Score 29; DB 2; Length 253;	
Best Local Similarity	71.4%; Pred. No. 3.5e+02;	
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	2 PXRPyXL 8	
Db	78 PARPyVL 84	
RESULT	15	
07P853	PRELIMINARY;	PRT; 257 AA.
ID	Q7P853	
AC	Q7P853;	
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DE	Acetyl-Coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).	
DE	Name=FNR2185;	
GN	Name=FNR2185;	
OS	Fusobacterium nucleatum subsp. vincentii ATCC 49256.	
OC	Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;	
OX	NCBI_TaxID=219982;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=TCC 49256;	
RA	Karpnata V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'souza M., Walunas T., Haelkorn R., Overbeek R., Kyrides N.;	
RA	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.	
RL	- - - CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	
DR	EMBL; BABF000005; EAA25081.1; -.	
DR	GO; GO:0009317; Clactetyl-CoA carboxylase complex; IEA.	
DR	GO; GO:003949; Fractetyl-CoA carboxylase activity; IEA.	
DR	GO; GO:0016874; F-transferase activity; IEA.	
DR	GO; GO:0016740; F:transferase activity; IEA.	
DR	GO; GO:0006633; P:fatty acid biosynthesis; IEA.	
DR	InterPro; IPR010195; Ac-CoA_carboxyla.	
DR	PFAM; PF03255; ACCA; 1	
DR	PRINTS; PR01069; ACCCTRFRASER.	
DR	TIGRFAMS; TIGR0013; acca; 1.	
KW	Complete proteome; Ligase; Transferase.	
SQ	SEQUENCE 312 AA; 34253 MW; 8DDE11C042DADA4 CRC64;	
Query Match	87.9%; Score 29; DB 2; Length 312;	
Best Local Similarity	71.4%; Pred. No. 4.4e+02;	
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	2 PXRPyXL 8	
Db	60 PDPRyAL 66	
RESULT	17	
07R99	PRELIMINARY;	PRT; 313 AA.
ID	Q7R99	
AC	Q7R99;	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Acetyl-Coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).	
DR	OrderedLocusNames=FNR0409;	
DR	Fusobacterium nucleatum (subsp. nucleatum).	
DR	Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;	
DR	TIGRFAMS; TIGR0013; acca; 1.	

OC Fusobacterium.
 OC NOB1_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21806394; PubMed=11889109;
 RT "genome sequence and analysis of the oral bacterium *Fusobacterium*
 RT nucleatum strain ATCC 25586.", DOI=10.1128/JB.184.7.2005-2018;2002;
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AB010527; AA194612.1; -.
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003389; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:000633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCIRFRASEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 DR KW Complete proteome; Ligase; Transferase.
 SQ Sequence 313 AA; 35303 MW; 878CFBC3F8DP261 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 313;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 62 PNRPyTL 68

RESULT 18

ID	ACCA_HABIN	STANDARD	PRT	315 AA.
ID	PA3872;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	25-OCT-2004 (Rel. 45, last annotation update)			
DE	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).			
GN	Name=accA; OrderedLocusNames=H10406;			
OS	Hemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.			
OC	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RD / KW20 / ATCC 51907;			
RX	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shizley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg J.D., Crotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Sudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Graham C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;			
RA	"whole genome random sequencing and assembly of <i>Haemophilus influenzae</i> RT Rd.", Science 269:496-512 (1995).			
CC	-!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA (By similarity). CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate + malonyl-CoA.			

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CC EMBL; U32724; AAC22055.1; -.
 DR PIR; 164065; 164065.
 DR TIGR; H10406; -.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCIRFRASEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 DR PROSITE; PSS0989; COA_CTE_CPER; 1.
 DR KW Complete proteome; Fatty acid biosynthesis; Ligase.
 SQ Sequence 315 AA; 35126 MW; E3B0B498A2686B23 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 315;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 66 PNRPyTL 72

RESULT 19

ID	ACCA_HABIN	PRELIMINARY	PRT	315 AA.
ID	Q886M7			
AC	Q886M7;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.			
GN	Name=accA; OrderedLocusNames=PST01550;			
OS	Pseudomonas syringae (Ipv; tomato).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.			
OC	NCBI_TaxID=323;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DC3000;			
RX	MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;			
RA	Buell C.R., Joardar V., Lindenberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haff D.H., Nelson W.C., Davidsen T.M., Zafer N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell B., Berry K.J., Utterback T.R., Van Alen S.E., Feldblyum T.V., D'Addezio M., Deng W.J., Ramos A.R., Almario J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Frazer C.M., Collier A.; Schneider D.J., Tang X., The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000.", Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).			
RA	DR EMBL; AB016861; AA055070.1; -. DR TIGR; PEP01550; -. DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA. DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA. DR GO; GO:0016740; F:transferase activity; IEA. DR GO; GO:0006633; P:fatty acid biosynthesis; IEA. DR InterPro; IPR001095; Ac-CoA_carboxylA. DR Pfam; PP03255; ACCA; 1.			

DR	PRINTS; PR01069; ACCCTTFRASEA.		
DR	TIGRFAMS; TIGR00513; accA; 1.		
KW	Complete proteome; Transferase.		
SQ	SEQUENCE 315 AA; 34975 MW; A878C54C71D5C555 CRC64;		
Qy	2 PXRPyXL 8		
Db	67 PLRPYTL 73		
RESULT 20			
Q8BMG4	PRELIMINARY;	PRT;	315 AA.
ID	Q8BMG4		
AC	Q8BMG4; -		
DT	01-JUN-2003 (TREMBrel. 24, Created)		
DT	01-JUN-2003 (TREMBrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)		
DB	Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.		
GN	Name=acca; Order=locusNames=PP1607;		
OS	Pseudomonas putida (strain KT2440);		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI_TaxID=160488;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2242060; PubMed=12534463;		
RA	Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Foultz D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapfle E.K., Scannlan D., Tran K., Moestl D., Moestl D., Weidler H., Lauber J., Stjepanovic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;		
RT	"Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.;"		
RL	Environ. Microbiol. 4:799-808 (2002).		
DR	EMBL; AS016779; AAN67228.1; -.		
DR	TIGR; PP1607; -.		
DR	GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.		
DR	GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.		
DR	GO: GO:005633; P:fatty acid biosynthesis; IEA.		
DR	InterPro; IPR010982; Lambda_Like_DNA.		
DR	InterPro; IPR010982; Lambda_Like_DNA.		
DR	InterPro; IPR010982; Lambda_Like_DNA.		
DR	PRINTS; PR01069; ACCCTTFRASEA.		
DR	PRINTS; PR01069; accA; 1.		
DR	TIGRFAMS; TIGR00513; accA; 1.		
DR	Complete proteome.		
SQ	SEQUENCE 315 AA; 35135 MW; 65952AE13959EDAD CRC64;		
Query Match	87.9%; Score 29; DB 2; Length 315;		
Best Local Similarity	71.4%; Pred. No. 4.5e+02;		
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	2 PXRPyXL 8		
Db	67 PLRPYTL 73		
RESULT 22			
Q9HKZ2	PRELIMINARY;	PRT;	316 AA.
ID	Q9HKZ2		
AC	Q9HKZ2; -		
DT	01-MAR-2001 (TREMBrel. 16, Created)		
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)		
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)		
DE	Acetyl-coenzyme A carboxylase carboxyl transferase (Alpha subunit);		
GN	Name=acab; Order=locusNames=PA06339;		
OS	Pseudomonas aeruginosa.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI_TaxID=287;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 15692 / PA01;		
RX	MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;		
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Micoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goletti L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;		
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.;"		
RL	Nature 406:939-944 (2000).		
DR	EMBL; AS004733; AAG07027.1; -.		
DR	PIR; DB3192; DB3192.		
DR	GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.		
DR	GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006633; P:fatty acid biosynthesis; IEA.		
DR	InterPro; IPR001095; AC-CoA_carboxyla.		

DR Pfam; PF0325; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFRAEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 316 AA; 34947 MW; 914D9418A79FB484 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 23

Q7VPL3 PRELIMINARY; PRT; 317 AA.

ID Q7VPL3
 AC Q7VPL3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 GN Name=acca; OrderedLocusNames=HD0051;
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteuelliaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=35000SP / ATCC 700724;
 RA Munson, R.S., Ray, W.C., Mahairas, G., Sabo, P., Mungur, R.,
 RA Johnson, L., Nguyen, D., Wang, J., Forst, C., Hood, L.;
 RT "The complete genome sequence of *Haemophilus ducreyi*";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE017151; AAP95066.1; -
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 DR GO; GO:003889; Fattyacyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016740; Ftranferase activity; IEA.
 DR GO; GO:0006633; P_fatty acid biosynthesis; IEA.
 DR InterPro; IPR01095; Ac-CoA carboxyla.
 DR InterPro; IPR01092; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR TIGRFAMS; TIGR00513; accA; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 317 AA; 35212 MW; 3DFB30A7680879C6 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 24

Q8D2H6 PRELIMINARY; PRT; 317 AA.

ID Q8D2H6
 AC Q8D2H6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE ACCA protein.
 GN Name=acca; OrderedLocusNames=WIGBR3780;
 OS Wiggleworthia glossinidia brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wiggleworthia.
 OX NCBI_TaxID=36870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2297718; PubMed=12219091; DOI=10.1038/ng986;
 RA Akhman, L., Yamashita, A., Watanabe, H., Ohshima, K., Shiba, T., Hattori, M.,

RA Akhoy, S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse files, *Wigglesworthia glossinidia*";
 RT Nat. Genet. 32:492-497(2003);
 RL Nat. Genet. 32:492-497(2003);
 DR EMBL; AB063522; BAC2424.1; -
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 GO; GO:0003889; Clacetyl-CoA carboxylase activity; IEA.
 GO; GO:0006633; P_fattyacyl acid biosynthesis; IEA.
 DR InterPro; IPR01095; Ac-CoA_carboxylA.
 DR InterPro; IPR010882; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFRAEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 KW Complete proteome.
 SQ SEQUENCE 317 AA; 35637 MW; 26588C43A815091B CRC64;

Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 25

Q9CNX9 PRELIMINARY; PRT; 317 AA.

ID Q9CNX9
 AC Q9CNX9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DR AccA.
 GN Name=acca; OrderedLocusNames=PM0292;
 OS Pasteuella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteuelliaceae; Pasteuella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=PM70;
 RA MEDLINE-21158566; PubMed=11248100; DOI=10.1073/pnas.051634598;
 RA May, B.J., Zhang, Q., Li, L.I., Paustian, M.L., Whittem, T.S., Kapoor, V.,
 RT "Complete genomic sequence of *Pasteuella multocida* PM70";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001);
 DR EMBL; AE006064; AAK02376.1; -
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003889; Clacetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P_fatty acid biosynthesis; IEA.
 DR InterPro; IPR001055; Ac-CoA carboxyla.
 DR InterPro; IPR000577; FGGY kin.
 DR InterPro; IPR01092; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFRAEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 317 AA; 35341 MW; F8B3DDA93723D1F6 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 26

ACCA_ECOLI STANDARD; PRT; 318 AA.

ID ACCA_ECOLI
 AC P30857;
 DT 01-JUL-1993 (Rel. 26, Created)

- DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 25-JAN-2005 (Rel. 46, last annotation update)
- DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE (EC 6.4.1.2).
- GN Name=accB; OrderedLocusName=b0185, 20197, ECS0187, SF0175, S0178;
- OS Escherichia coli,
Escherichia coli O157:H7, and
Shigella flexneri.
- OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
- OX NCBI_TaxID=562, 83334, 623;
- RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE..
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RX MEDLINE=92380982; PubMed=1355089;
- RA Li, S.-J.; Cronan, J. E. Jr.;
- RT "The genes encoding the two carboxyltransferase subunits of
Escherichia coli acetyl-CoA carboxylase.";
- RL J. Biol. Chem. 267:16841-16847(1992).
- RN [2] SEQUENCE FROM N.A..
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
- RA Yamamoto, Y.; Submitted (DPC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3] SEQUENCE FROM N.A..
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=978503; DOI=10.1126/science.277.5331.1453;
- RA Blattner, F.R.; Plunkett, G. III; Bloch, C.A.; Perna, N.T.; Burland, V.;
 RA Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.;
 RA Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Geeden, M.A.; Rose, D.J.,
 RA Mau, B.; Shao, Y.;
 RL Science 277:1453-1474(1997).
- RN [4] SEQUENCE FROM N.A..
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RA Yamamoto, K.; Mori, H.; Murayama, N.; Kataoka, K.; Yano, M.; Itoh, T.;
 RA Inokuchi, H.; Maki, T.; Hatada, E.; Fukuda, R.; Ichihara, S.,
 RA Mizuno, T.; Makino, K.; Nakata, A.; Yura, T.; Sampei, G.; Mizobuchi, K.;
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the
 RT 4.0 - 6.0 min (189,987 - 281,416pp) region";
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [5] SEQUENCE FROM N.A..
 RC SPECIES=E.coli;
- RA Schramm, S.; Duncan, M.; Allen, B.; Araujo, R.; Aparicio, A.; Chung, E.;
 RA Lashkari, D.; Lew, H.; Lin, D.; Namath, A.; Oesther, P.; Roberts, D.;
 RA Davis, R.W.; Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [6] SEQUENCE FROM N.A..
 RP SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35050409;
- RA Perna, N.T.; Plunkett, G. III; Burland, V.; Mau, B.; Glasner, J.D.; Darling, A.;
 RA Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.;
 RA Pfeifer, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.;
 RA Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.T.; Potamitis, K.;
 RA Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.;
 RA Welch, R.A.; Blattner, F.R.;
 RT "Genome Sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
- RN [7] SEQUENCE FROM N.A..
 RP SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RTMD 0509952 / EHEC;
 RX MEDLINE=21515231; PubMed=11258796;
- RA Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.,
 RA Iida, T.; Takami, H.; Honda, T.; Sakakawa, C.; Ogasawara, N.; Yasunaga, T.,
 RA Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; Shinagawa, H.;
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 RT 0157:H7 and genomic comparison with a laboratory strain K-12.";
- RL DNA Res. 8:11-22(2001).
 RN [8] SEQUENCE OF 163-318 FROM N.A..
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RX MEDLINE=9736816; PubMed=9226257;
- RA Kikuchi, Y.; Kojima, H.; Tanaka, T.; Takatsuka, Y.; Kamio, Y.;
 RT "Characterization of a second lysine decarboxylase isolated from
Escherichia coli.";
- RL J. Bacteriol. 179:4486-4492(1997).
- RN [9] SEQUENCE OF 1-12..
 RC SPECIES=E.coli; STRAIN=K12 / EMG32;
 RX MEDLINE=97433975; PubMed=9298645;
- RA Link, A.J.; Robison, K.; Church, G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
- RN [10] SEQUENCE FROM N.A..
 RC SPECIES=S.Flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384530; DOI=10.1093/nar/gkf565;
- RA Jin, Q.; Yuan, Z.; Xu, J.; Wang, Y.; Shen, Y.; Lu, W.; Wang, J.; Liu, H.;
 RA Yang, J.; Yang, F.; Zhang, X.; Zhang, J.; Yang, G.; Wu, H.; Qu, D.; Dong, J.,
 RA Sun, L.; Xue, Y.; Zhao, A.; Gao, Y.; Zhu, J.; Kan, B.; Ding, K.; Chen, S.,
 RA Cheng, H.; Yao, Z.; He, B.; Chen, R.; Ma, D.; Qiang, B.; Wen, Y.; Hou, Y.,
 RA Yu, J.;
 RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
 through comparison with genomes of *Escherichia coli* K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
- RN [11] SEQUENCE FROM N.A..
 RC SPECIES=S.Flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
- RA DOI=10.1128/JAI.71.5.2775-2786.2003;
- RA Wei, J.; Goldberg, M.B.; Burland, V.; Venkatesan, M.M.; Deng, W.;
 RA Fournier, G.; Mayhew, G.F.; Plunkett, G. III; Rose, D.J.; Darling, A.;
 RA Mau, B.; Perna, N.T.; Payne, S.M.; Runyan-Janecky, L.J.; Zhou, S.;
 RA Schwartz, D.C.; Blattner, F.R.;
 RT "Complete genome sequence and comparative genomics of *Shigella*
flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
- CC CC -I- FUNCTION: This protein is a component of the acetyl coenzyme A
 CC CC carboxylase complex; first, biotin carboxylase catalyzes the
 CC CC carboxylation of the carrier protein and then the transcarboxylase
 CC CC transfers the carboxyl group to form malonyl-CoA.
 CC CC -I- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) (-) = APP + phosphate
 CC CC + malonyl-CoA.
 CC CC -I- SUBUNIT: Acetyl-CoA carboxylase is an heterohexameric of biotin
 CC CC carboxyl carrier protein, biotin carboxylase and the two subunits
 CC CC of carboxyl transferase in a 2:2 complex.
 CC CC -I- SIMILARITY: Belongs to the accA family.
 CC CC -I- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter
 CC CC domain.
- CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC CC the European Bioinformatics Institute. There are no restrictions on its
 CC CC use by non-profit institutions as long as its content is in no way
 CC CC modified and this statement is not removed. Usage by and for commercial
 CC CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC CC or send an email to license@isb-sib.ch).
- DR EMBL; M06394; AAC03701; -
 DR EMBL; D03536; BA07860_1; -
 DR EMBL; U00096; AAC03296_1; -
 DR EMBL; D03536; BA07860_1; -
 DR EMBL; U070214; AA080614_1; -
 DR EMBL; AB005194; AAQ5487_1; -
 DR EMBL; AB002550; BA033610_1; -
 DR EMBL; D07518; BA21655_1; -
 DR EMBL; AB015054; AAC41337_1; -
 DR EMBL; AB016978; AAP15718_1; -

DR PIR; A43452; A43452.
 DR C85503; C85503.
 DR PIR; C90652; C90652.
 DR EchoBASE; EB1600; -.
 DR Ecogene; EG11647; acca.
 DR InterPro; IPR001095; Ac-CoA _ carboxylyA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCUTRFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 DR PROSITE; PSS0989; COA CT CTER; 1.
 KW Complete proteome; Direct protein sequencing; Fatty acid biosynthesis; Ligase.
 FT INIT_MER 0 0
 FT DOMAIN 83 118
 FT DOMAIN 24 24
 FT CONFLICT 318 AA; 35110 MW; 8938B08E5D3C9AD CRC64;
 SQ Query Match Best Local Similarity 87.9%; Score 29; DB 1; Length 318;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRXPXL 8
 Db 69 PORPYTL 75
 RESULT 27
 ACCA_SALTY STANDARD; PRT; 318 AA.
 ID ACCA_SALTY
 AC P0674;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE (EC 6.4.1.2).
 GN Name=acca; OrderedLocusNames=STM0232, STY0255, t0233;
 OS *Salmonella typhimurium*, and
 OS *Salmonella* Typhi.
 OC Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC *Salmonellaceae*; *Salmonella*.
 RN [1]
 RP Sequence from N.A.
 RC SPECIES=S.TYPHIMURIUM; STRAIN=LIT2 / SGSC112 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=1677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvane E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stonking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LIT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP Sequence of 1-35 from N.A.
 RC SPECIES=S.TYPHIMURIUM;
 RX MEDLINE=90008797; PubMed=2676978;
 RA Lancy E.D., Lifschis M.R., Munson P., Maurer R.;
 RT "Nucleotide sequence of dnaB, the gene for the polymerase subunit of DNA polymerase III in *Salmonella typhimurium*, and a variant that facilitates growth in the absence of another polymerase subunit.";
 RT J. Bacteriol. 171:5581-5586(1989).
 RL
 RN [3]
 RP Sequence from N.A.
 RC SPECIES=S.TYPHI; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.B., Thomson D., Holden M.T.G., Sebaihia M.,
 RA Churcher C.M., Mungall K.L., Bentley D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moile S., O'Gaoar P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella* enterica serovar Typhi CT18.";
 RT Nature 413:848-852(2001).
 [4]
 RN Sequence from N.A.
 RC SPECIES=S.TYPHI; STRAIN=TY2 / ATCC 700931;
 RC MEDLINE=22331367; PubMed=126450;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyani V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of *Salmonella enterica* enterica serovar Typhi strains TY2 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RC -!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA.
 CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -!- SUBUNIT: Acetyl-CoA carboxylase is an heterohexamer of biotin carboxyl carrier protein, biotin carboxylase and the two subunits of carboxyl transferase in a 2:2 complex.
 CC -!- SIMILARITY: Belongs to the acca family.
 CC -!- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.ebi-sib.ch/announce/> or send an email to license@ebi-sib.ch).
 CC -----
 DR EMBL; AB008705; RAL19196.1; -.
 DR EMBL; M26046; -, NOT_ANNOTATED_CDS.
 DR EMBL; AU627266; CRD0890.1; -.
 DR EMBL; AB16834; RAO67963.1; -.
 DR StyGene; SG10496; acca.
 DR InterPro; IPR00195; Ac-CoA_carboxylyA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCUTRFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 DR PROSITE; PSS0989; COA CT CTER; 1.
 KW Complete proteome; Fatty-acid biosynthesis; Ligase.
 FT INIT_MER 0 0
 FT DOMAIN 83 118
 FT DOMAIN 16 16
 FT CONFLICT 318 AA; 35212 MW; 749B990EC01F9D0 CRC64;
 SQ Query Match Best Local Similarity 87.9%; Score 29; DB 1; Length 318;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRXPXL 8
 Db 69 PORPYTL 75
 RESULT 28
 Q667KS PRELIMINARY; PRT; 319 AA.
 ID Q667KS
 AC 0667KS
 DT 25-OCT-2004 (TREMBREL_28, Created)
 DT 25-OCT-2004 (TREMBREL_28, Last sequence update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit al. . . (EC 6.4.1.2).
 DE Name=acca; ORFNames=YPRB2977;
 OG *Versinia pseudotuberculosis* IP 32953.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=273123;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TP 32253;
 RX PubMed=15358958;
 RA Chain P.S.G., Carmel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regal M.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
 RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.,
 RT "Insights into the genome evolution of *Yersinia pestis* through whole
 genome comparison with *Yersinia pseudotuberculosis*."
 Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 RL DR GO: GO:0016874; F-ligase activity; IEA.
 DR GO: GO:001069; Ac-CoA carboxylase.
 DR InterPro: IPR001035; Ac-CoA carboxylase.
 DR GO: GO:0016740; F-ligase activity; IEA.
 DR GO: GO:0016874; F-ligase activity; IEA.
 DR Pfan: PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCTFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Ligase; Transferase.
 SQ SEQUENCE 319 AA; 35495 MW; 45ABB190ECB7B402E CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 DR Do 70 PRRPyTL 76
 RESULT 29
 Q8PAW9 PRELIMINARY; PRT; 319 AA.
 ID Q8PAW9
 AC Q8PAW9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DB Acetyl-coenzyme A carboxylase carboxyl transferase.
 GN Name=acca; OrderedLocusNames=XACI357;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=2022145; PubMed=15024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Victorino C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bartolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camanava F., Cardozo J., Chambergo F., Cipolla L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Curitino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreria R.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi J.A.D., Sena J.A.D., Silva Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kajimura J.P.,
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing
 host specificities."
 RT Nature 417:459-463 (2002).
 DR EMBL; AB012234; AAM40551; -.
 DR GO: GO:0009317; Cl-acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003899; Fatty-acyl-CoA carboxylase activity; IEA.
 DR Getubal J.C., Kitajima J.P.,
 RA Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi J.A.D., Sena J.A.D., Silva Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing
 host specificities."
 RT Nature 417:459-463 (2002).
 DR EMBL; AB012234; AAM40551; -.
 DR GO: GO:0009317; Cl-acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003899; Fatty-acyl-CoA carboxylase activity; IEA.
 DR GO: GO:0006633; P-fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Lambda_like_DNA.
 DR InterPro: IPR010882; Lambda_like_DNA.
 DR Pfan: PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCTFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome.
 SQ SEQUENCE 319 AA; 35270 MW; 385DBBBABEA0DC3 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Q8ZH52 PRELIMINARY; PRT; 319 AA.
 ID Q8ZH52; QTMH6; PRELIMINARY; PRT; 319 AA.
 AC QTMH6;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2) [Acetyl CoA carboxylase, carboxytransferase component, alpha subunit]; OrderedLocusNames=YP2790, YP0160, Y3119;
 DE subunit); Name=acCA; OrderedLocusNames=YP2790, YP0160, Y3119;
 GN OS Yersinia pestis.
 OC Yersinia pestis, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia.
 OC NCBI_TaxID=632;
 RN [1] RP SEQUENCE FROM N.A.
 RC STRAIN=GO_92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RX Parkhill J., Wren B.W., Thomson N.R., Titchall R.W., Holden M.T.G., Prentice M.B., Sebastian M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley D., Brooks J., Cardeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Immonds M., Moulle S., Oyston P.C.F., Peacock S., Quail M.A., Rutherford K.K.M., Perry R.D.; "Genome sequence of *Yersinia pestis*, the causative agent of plague.", Nature 413:523-527(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis; MEDLINE=2217863; PubMed=12142430;
 RX DOI=10.1128/JB.146.14601-4611.2002;
 RA Dang W., Bland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fletcherston J.D., Lindner L.B., Brubaker R.R., Piano G.V., Straley S.C., McDonough M.L., Matson J.S., Blattner F.R., RA Perry R.D.; "Genome sequence of *Yersinia pestis* KIM.", RT J. Bacteriol. 184:4601-4611(2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D., Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., RA Yang R.; Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RL DR EMBL; AU41446; CACB89902.1; -. DR EMBL; AE013912; AMB6669.1; -. DR PTB; AE017137; AAS62974.1; -. DR PIR; AC0130.
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; P:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016874; Filigase activity; IEA.
 DR GO; GO:0016740; F-transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR PRINTS; PRO1069; ACCCUTRFRASEA.
 DR TIGRFAMS; TIGR00513; acCA; 1.
 KW Complete proteome; Lipase; Transferase.
 SQ SEQUENCE 319 AA; 35595 MW; 45ABBL90ECTB402E CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02; Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 33
 QTMH6 PRELIMINARY; PRT; 319 AA.
 ID QTMH6; PRELIMINARY; PRT; 319 AA.
 AC QTMH6;
 DT 01-MAR-2004 (TREMBrel. 26, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Acetyl-CoA carboxylase alpha subunit; Name=acCA; OrderedLocusNames=plu0688;
 OS Photorhabdus luminescens (subsp. laumondii); Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
 OC NCBI_TaxID=141679;
 RN [1] RP SEQUENCE FROM N.A.
 RC STRAIN=TT01; MEDLINE=2295627; PubMed=14528314;
 RA Duchaud E., Rustin C., Frangeul L., Buchrieser C., Givaudan A., Taourt S., Bocs S., Bourlaux-Eude C., Chandler M., Charles J.-F., Dausse E., Derouze R., Derzelje S., Fryssinet G., Gaudriault S., RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V., Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.; "The genome sequence of the entomopathogenic bacterium Photorhabdus luminescens"; Nat. Biotechnol. 21:1207-1213 (2003).
 RL DR EMBL; BX571861; CAE12383.1; -. DR Photolist; plu0688; -. DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; P:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; acCA; 1.
 PRINTS; PRO1069; ACCCUTRFRASEA.

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02; Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0; RT luminescens"; Nat. Biotechnol. 21:1207-1213 (2003).
 DR EMBL; BX571861; CAE12383.1; -. DR Photolist; plu0688; -. DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; P:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; acCA; 1.
 PRINTS; PRO1069; ACCCUTRFRASEA.

RESULT 32
 QTMH6

DR TIGRFAMs; TIGR00513; accA; 1.
 KW Complete proteome.
 SQ SEQUENCE 319 AA; 35523 MW; EIF08BF0F45FCE2 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 34
 OYVRD0 PRELIMINARY; PRT; 319 AA.

ID QYVRD0; PRELIMINARY; PRT; 319 AA.

AC QYVRD0; PRELIMINARY; PRT; 319 AA.

DT 01-OCT-2003 (TREMBIrel. 25, Created)
 DT 01-OCT-2003 (TREMBIrel. 25, Last sequence update)

DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).

DB 6.4.1.2.

GN Name=accA; OrderedlocusName=Bf1287;

OS Candidatus Blochmannia floridanus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.

RN [1]

RP SEQUENCE FROM N.A.

DR MEDLINE-22784745; PubMed=12886019; DOI=10.1073/pnas.1533499100;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
 RA Latorre A., Rausell C., Kammerbeek J., Gadau J., Hoedlboier B.,
 RA van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of *Blochmannia floridanus*: comparative analysis
 of reduced genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9389-9393 (2003).
 DR EMBL; BX248585; CAD83388.1; -.

DR GO; GO:0009317; C-acetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; F-acetyl-CoA carboxylase activity; IEA.

DR GO; GO:0006633; F-fatty acid biosynthesis; IEA.

DR InterPro; IPR01035; Ac-CoA_carboxyla.

DR Pfam; PF03255; accA; 1.

DR TIGRFAMs; TIGR00513; accA; 1.

KW Complete proteome.

SQ SEQUENCE 319 AA; 35813 MW; 1DB9B1C7CCEA3A9C CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 35
 O87MR3 PRELIMINARY; PRT; 319 AA.

ID O87MR3; PRELIMINARY; PRT; 319 AA.

AC O87MR3; PRELIMINARY; PRT; 319 AA.

DT 01-JUN-2003 (TREMBIrel. 24, Created)
 DT 01-JUN-2003 (TREMBIrel. 24, Last sequence update)

DE Acetyl-CoA carboxylase, carboxyl transferase alpha subunit.

GN OrderedlocusName=VP23102;

OS *Vibrio parahaemolyticus*;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibionaceae; Vibrio.

RN [1]

RP SEQUENCE FROM N.A.

DR STRAIN=RIMD 2210633 / serotype O3:K6;
 DR MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RA Makino K., Ohshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Nakima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 RT distinct from that of *V. cholerae*";
 RL Lancet 361:743-749 (2003).
 DR EMBL; AP005081; BAC6065.1; -.

DR GO; GO:0009317; C-acetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; F-acetyl-CoA carboxylase activity; IEA.

DR GO; GO:0016740; F-transf erase activity; IEA.

DR GO; GO:0006633; F-fatty acid biosynthesis; IEA.

DR InterPro; IPR01035; Ac-CoA_carboxyla.

DR InterPro; IPR01095; Lambda_Like_DNA.

DR Pfam; PF03255; accA; 1.

DR PRINTS; PRO1069; ACCCFPRASBA.

DR TIGRFAMs; TIGR00513; accA; 1.

KW Complete proteome.

SQ SEQUENCE 319 AA; 35699 MW; 31P99366BE2A4667 CRC64;

QY 2 PXRPYXL 8
 ID Q8JUFO | ||| |
 Db 67 PORPYTL 73

RESULT 40

Q8JUFO PRELIMINARY; PRT; 319 AA.

ID Q8JUFO; PRELIMINARY; PRT; 319 AA.

AC Q8JUFO; PRELIMINARY; PRT; 319 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Putative acetyl-CoA carboxylase carboxyl transferase subunit (BC
 6.4.1.2).

GN Name=acCA; OrderedLocusNames=NMA1349;

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN {1}

RP SEQUENCE FROM N.A.

RC STRAIN=22491 / Serogroup A / Serotype 4M;

RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;

RA Parkhill J.; Achtman M.; James K.D.; Bentley S.D.; Churcher C.M.;
 RA Klee S.R.; Morelli G.; Basham D.; Brown D.; Chillingworth T.;
 RA Davies R.M.; Davis P.; Devlin K.; Feltwell T.; Hamlin N.; HoIroyd S.;
 RA Jigels K.; Leather S.V.; Moule S.; Mungall K.L.; Quail M.A.;
 RA Rajandream M.A.; Rutherford K.M.; Simmonds M.; Skelton J.;
 RA Whitehead S.; Spratt B.G.; Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491.";
 RL Nature 404:502-506(2000).

DR IEMBL; AU162755; CAB84596.1; -.

DR PIR; H81901; H81903.

DR GO; GO:0009317; Facetetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; Facetetyl-CoA carboxylase activity; IEA.

DR GO; GO:0016874; F-ligate activity; IEA.

DR GO; GO:0011670; Fattytransferase activity; IEA.

DR GO; GO:0006633; Fatty acid biosynthesis; IEA.

DR InterPro; IPR001095; Ac-CA_carboxyla.

DR Pfam; PF03255; ACCA; 1.

DR PRINTS; PR01069; ACCATPASEA.

DR TIGRFAMS; TIGR00513; acCA; 1.

KW Complete proteome; Ligase; transferase.

SQ SEQUENCE 319 AA; 35492 MW; EA753CDSE169BCB0 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e-02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
 ID Q8JUFO | ||| |
 Db 67 PORPYTL 73

Search completed: March 28, 2005, 08:37:17
 Job time : 124 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model
Run on: March 28, 2005, 08:33:43 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-10-036-918B-4

Perfect score: 33

Sequence: 1 XPKRPyXL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 100 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	90.9	360 2 H97447	probable ferredoxin
2	30	90.9	360 2 A12655	ferritin I Atu07
3	30	90.9	1100 2 S43677	protein tyrosine k
4	29	87.9	253 1 C47031	orf1_3' of bah - st
5	29	87.9	312 2 A81399	acetyl-coa carboxy
6	29	87.9	315 2 I64065	acetyl-CoA carboxy
7	29	87.9	316 2 D83192	acetyl-coenzyme A
8	29	87.9	319 1 A43452	acetyl-coA carboxy
9	29	87.9	319 2 AB0531	acetyl-coenzyme A
10	29	87.9	319 2 H82836	probable acetyl-Co
11	29	87.9	319 2 H81903	acetyl-coA carboxy
12	29	87.9	319 2 BB1119	tachykinin receptor
13	29	87.9	319 2 C90652	prolyl endopeptidase
14	29	87.9	319 2 C85503	ragC protein - Bra
15	29	87.9	319 2 F82100	acetyl-coA carboxy
16	29	87.9	319 2 AC0130	methane sulfonate s
17	29	87.9	385 2 A12959	tachykinin receptor
18	29	87.9	385 2 E9832	prolyl endopeptidase
19	29	87.9	504 2 A41783	ragC protein - Bra
20	29	87.9	685 2 B75257	protein tyrosine k
21	29	87.9	1060 2 T31341	neurotensin - bovi
22	29	87.9	1099 2 S48053	stringent starvati
23	28	84.8	13 1 UNBO	stringent starvati
24	28	84.8	150 2 D64123	stringent starvati
25	28	84.8	158 2 F82305	stringent starvati
26	28	84.8	165 2 E91141	stringent starvati
27	28	84.8	165 2 JS0666	stringent starvati
28	28	84.8	165 2 H88598	stringent starvati
29	84.8	166 2 ADD908	stringent starvati	

ALIGNMENTS

RESULT 1
H9747 probable ferredoxin (PA5411) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C;Species: Agrobacterium tumefaciens
 C;Accession: S43677 2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;DATE: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: H9747
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Iappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
 A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A;Reference number: A97359; MUID:21608551; PMID:1743194
 A;Accession: H9747
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <KUR>
 A;Cross-references: UNIPROT:Q8UHR5; GB:AE07869; PIDN:AAK86537.1; PID:915155697; GSPDB:G
 C;Genetics:
 A;Gene: AGR_C_1321
 A;Map position: circular chromosome
 C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredoxin
 Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPPXYL 8
 Db 77 PSRPPYAL 83

RESULT 2
 A12665 ferredoxin I Atu0727 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Accession: A12665 2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Peter, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: A12665
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <KUR>
 A;Cross-references: UNIPROT:Q8UHR5; GB:AE008688; PIDN:AAL41743.1; PID:917739094; GSPDB:G
 C;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0727
 A;Map position: circular chromosome
 C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredoxin
 Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPPXYL 8
 Db 77 PSRPPYAL 83

RESULT 3
 S43677 protein tyrosine kinase JAK3 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
 C;Accession: S43677

Query Match 87.9%; Score 29; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 60 PDRPyAL 66

RESULT 6

I4065 acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase alpha chain - *Haemophilus influenzae*
 C;Species: *Haemophilus influenzae*
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C;Accession: I4065
 R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. D.-M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: I4065
 A;Status: nucleic acid sequence, not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-315 <TIGR>
 A;Cross-references: UNIPROT:P43872; GB:U32724; GB:L42023; NID:91573378; PIDN: AAC22065.1;
 C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
 C;Keywords: fatty acid biosynthesis; ligase

Query Match 87.9%; Score 29; DB 2; Length 315;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 66 PNRPyTL 72

RESULT 7

D33192 acetyl-coenzyme A carboxyl transferase (alpha subunit) PA3639 [imported] - E
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: D33192
 R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brachman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: AB2950; MUID:20437337; PMID:10984043
 A;Accession: D33192
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-316 <STO>
 A;Cross-references: UNIPROT:Q9HXZ2; GB:AE004783; GB:AE004091; NID:9949786; PIDN: AAC0702
 A;Experimental source: strain PA01
 C;Gene: accA; PA3639
 C;Superfamily: acetyl-CoA carboxyl transferase alpha chain
 Query Match 87.9%; Score 29; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 67 PKRPYTL 73

RESULT 8

A43452

RESULT 9

AB0531 acetyl-coenzyme A carboxyl transferase chain alpha [imported] - *Salmonella enterica* serovar Typhi
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0531
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Barral, S.; Moule, S.; O'Gara, P.; Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0531
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-319 <PAR>	A;Cross-references: GB:AL1513382; PIDN:CAD08690.1; PID:g16501513; GSPDB:GN00176
C;Genetics:	A;Experimental source: serogroup A, strain 22491
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	A;Gene: accA; NMA1349
C;Keywords: ligase	C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
Query Match	Query Match
Best Local Similarity 87.9%; Pred. No. 69; Length 319;	Best Local Similarity 87.9%; Pred. No. 69; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8	Qy 2 PXRPyXL 8
Db 70 PQRPYTL 76	Db 67 PQRPYTL 73
RESULT 10	RESULT 12
H82836 acetyl-coenzyme A carboxyl transferase subunit alpha xfo203 [imported] - Xyl	B81119 acetyl-CoA carboxylase, carboxyl transferase alpha chain NMB1139, NMB1177 [imported] - Ne
C;Species: Xylella fastidiosa	C;Species: Neisseria meningitidis
C;Accession: H82836	C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
N;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer	C;Accession: B81119; G81114
A;Title: The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .	R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hsu, H.; Qin, H.; Yamashita, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
A;Reference number: A82515; MUID:20365717; PMID:10910347	Science 287, 1809-1815, 2000
A;Note: for a complete list of authors see reference number A59328 below	A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Accession: H82836	A;Title: Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58.
A;Status: preliminary	A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Molecule type: DNA	A;Accession: B81119
A;Residues: 1-319 <SIM>	A;Molecule type: DNA
A;Experimental source: strain 945C	A;Residues: 1-319 <TER>
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aceacio, M.; Alvarenga, R.; A	A;Cross-references: UNIPROT:Q9URV8; GB:AE002462; GB:AE002098; NID:97226363; PIDN:AAF4152;
Briones, M.R.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H	A;Experimental source: serogroup B, strain MC58
A;Authors: Martins, E.M.F.; Matsukawa, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyake, C.Y.; P	A;Accession: B81114
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeiro, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaya, M.	A;Molecule type: DNA
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva Jr., W.A.; da Silva, A.M.; Tsukamoto, M.;	A;Residues: 1-319 <TER>
A;Reference number: A59328	A;Cross-references: GB:AB002465; GB:AE002098; NID:97226401; PIDN:AAF41562.1; PID:97226414
A;Contents: annotation	A;Experimental source: serogroup B, strain MC58
C;Genetics:	C;genetics:
A;Gene: XF0203	A;Gene: NMB1139; NMB1177
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
Query Match	Query Match
Best Local Similarity 87.9%; Score 29; DB 2; Length 319;	Best Local Similarity 87.9%; Score 29; DB 2; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8	Qy 2 PXRPyXL 8
Db 67 PQRPYTL 73	Db 67 PQRPYTL 73
RESULT 11	RESULT 13
H81903 probable acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain NMA1349 [si	C90652 acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain - Escherichia coli (e
C;Species: Neisseria meningitidis	C;Species: Escherichia coli
C;Accession: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004	C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H81903	C;Accession: C90652
R;Parikh, J.; Achitman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
; Hollroyd, S.; Jacobs, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,	gakawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
Nature 404, 502-505, 2000	A;Residues: 8-112, 2001
A;Title: Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 22491.	A;Cross-references: UNIPROT:P30067; GB:BA000007; PIDN:BA033610.1; PID:g13359643; GSPDB:GN
A;Reference number: A81775; MUID:20222556; PMID:10761919	A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Accession: H81903	A;Accession: C90652
A;Status: preliminary	A;Status: preliminary
A;Molecule type: DNA	A;Molecule type: DNA
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	A;Residues: 1-319 <DNA>

Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58, Strain R1
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E98323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <KUR>
A;Cross-references: UNIPROT:Q8UAT8; GB:AE007870; PIDN:AAK90111.1; PID:g15160102; GSPDB:G
C;Genetics:
A;Gene: AGR_L_3078
A;Map position: linear chromosome

RESULT 19
Query Match 87.9%; Score 29; DB 2; Length 385;
Best Local Similarity 71.4%; Pred. No. 85; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 171 PAPPyNL 177

RESULT 19
tachykinin receptor NKD - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A41783
R;Monnier, D.; Colas, J.-F.; Rosay, P.; Hen, R.; Borrelli, E.; Marteaux, L.
J. Biol. Chem. 267, 1288-1302, 1992
A;Title: NKD, a developmentally regulated tachykinin receptor in *Drosophila*.
A;Reference number: A41783; MUID:92112776; PMID:1370464
A;Accession: A41783
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-504 <MON>
A;Note: Sequence extracted from NCBI backbone (NCBIP:76545)
C;Genetics:
A;Gene: FlyBase:Takr86C
A;Cross-references: FlyBase:FBgn0004841
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 87.9%; Score 29; DB 2; Length 504;
Best Local Similarity 71.4%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 72 PTRPyEL 78

RESULT 20
prolyl endopeptidase - *Deinococcus radiodurans* (strain R1)
C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75267
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Mau, M.; Shem, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Accession: B75267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <WHT>
A;Cross-references: EMBL:132955
R;Mittnun, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
submitted to the EMBL Data Library, August 1994
A;Reference number: S51607
A;Accession: S51607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, R'62-1099 <W12>
A;Cross-references: EMBL:132955; NID:9529238; PIDN:AA21565.1; PID:9529239
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;915-1093/Domain: protein kinase homology <KIN1>
F;824-832/Region: protein kinase ATP-binding motif

Query Match 87.9%; Score 29; DB 2; Length 1099;
Best Local Similarity 71.4%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 396 PSRPyRL 402

RESULT 21
T31341
rgc protein - *Bradyrhizobium japonicum*
C;Species: *Bradyrhizobium japonicum*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31341
R;Narberhaus, F.; Krummenacher, P.; Fischer, H.M.; Hennecke, H.
Mot. Microbiol. 24, 93-104, 1997
A;Title: Three disparately regulated genes for sigma32-like transcription factors in Bracillus
A;Reference number: 221007; MUID:9788751; PMID:9140968
A;Accession: T31341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1060 <WXR>
A;Cross-references: UNIPROT:O69238; EMBL:AJ225023; NID:92961292; PIDN:CAA12353.1; PID:921007
C;Genetics:
A;Gene: rggC
C;Superfamily: cation efflux system membrane protein czcA
Query Match 87.9%; Score 29; DB 2; Length 1060;
Best Local Similarity 71.4%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 615 PAPPyNL 621

RESULT 22
S48053
protein tyrosine kinase - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Aug-2004
C;Accession: S48053; MUID:551607
R;Mittnun, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
Nature 370, 153-157, 1994
A;Title: Involvement of the Jak-3 Janus kinase in signalling by interleukins 2 and 4 in T
A;Reference number: S48053; MUID:94294024; PMID:8022486
A;Accession: S48053
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1099 <W1T>
A;Cross-references: EMBL:132955
R;Mittnun, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
submitted to the EMBL Data Library, August 1994
A;Reference number: S51607
A;Accession: S51607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, R'62-1099 <W12>
A;Cross-references: EMBL:132955; NID:9529238; PIDN:AA21565.1; PID:9529239
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;914-1093/Domain: protein kinase homology <KIN1>
F;824-832/Region: protein kinase ATP-binding motif

Query Match 87.9%; Score 29; DB 2; Length 1099;
Best Local Similarity 71.4%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 396 PSRPyRL 402

Db 228 PGRPYAL 234
 R;Heidelberg, J.F.; Eben, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Brmlaeva, M.D.; Vamathevan, J.; Basa, S.; Qin, H.; Dragoi, I.; Sellers, P.
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995
 UNBO
 RESULT 23
 A;Title: neurotensin - bovine
 A;Reference number: A92035; MUID:20406833; PMID:10952301
 A;Accession: P82305
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-13 <C&R>
 A;Experimental source: hypothalamus
 R;Carraway, R.; Leeman, S.E.
 J. Biol. Chem. 250, 1907-1911, 1975
 A;Title: The amino acid sequence of a hypothalamic peptide, neurotensin.
 A;Reference number: A92172; MUID:75095678; PMID:1167549
 A;Accession: A01420
 A;Molecule type: protein
 A;Residues: 1-13 <C&R>
 A;Content: annotation; synthesis
 A;Note: a tridecapeptide chemically and pharmacologically identical with the natural peptide
 C;Keywords: neuropeptide; pyroglutamatic acid
 F1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match 84.8%; Score 28; DB 1; Length 13;
 Best Local Similarity 71.4%; Pred. No. 3.7;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 7 PRPYYL 13

RESULT 24
 Db4123
 stringent starvation protein sspB - Haemophilus influenzae (strain Rd KW20)
 C;Species: Haemophilus influenzae
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 12-Jul-2004
 CAccession: D64123
 R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weilman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
 A;Authors: Graham, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: D64123
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-150 <TIGR>
 A;Cross-references: UNIPROT:P45206; GB:U32822; GB:L42023; NID:91574265; PIDN: AAC23089.1; C;Genetics:
 A;Gene: sspB
 C;Superfamily: Clpx-specific adaptor protein SspB

RESULT 25
 P82305
 stringent starvation protein B vc0577 [imported] - Vibrio cholerae (strain N16961 serogr
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
 C;Accession: P82305

Query Match 84.8%; Score 28; DB 2; Length 150;
 Best Local Similarity 71.4%; Pred. No. 51; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 2 PXRPyXL 8
 Db 7 PRPYYL 13

RESULT 26
 E91141
 stringent starvation protein B [imported] - Escherichia coli (strain O157:H7, substrain F)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
 CAccession: E91141
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., Gabawara, N.; Yabunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: E91141
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-165 <HAY>
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 A;Cross-references: UNIPROT:P25663; GB:BA000007; PIDN:BAB37524.1; PID:913363574; GSPDB:GN
 C;Genetics:
 A;Gene: EC04101
 C;Superfamily: Clpx-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 165;
 Best Local Similarity 71.4%; Pred. No. 56; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 2 PXRPyXL 8
 Db 8 PRPYYL 14

RESULT 27
 JS0666
 stringent starvation protein B, sspB - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 12-Jul-2004
 CAccession: JS0666; FF5114
 R;Williams, M.D.; Fuchs, J.A.; Flickinger, M.C.
 Gene 109, 21-30, 1991
 A;Title: Null mutation in the stringent starvation protein of Escherichia coli disrupts JI
 A;Reference number: JS0666; MUID:92097948; PMID:1721886
 A;Accession: JS0666
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-165 <WIL>
 A;Cross-references: UNIPROT:P25663; GB:ME0208; NID:9147871; PIDN:AAA24650.1; PID:9147872
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, J.A.; Rose, D.J.; Mau, B.; Shao, Y.

R;Regul: Pect. 14, 313-321, 1986
 A;Title: Isolation and characterization of a neuropeptidyl-like decapeptide from a canine
 A;Reference number: A60324; MUID:86314883; PMID:3749527
 A;Accession: A60324
 A;Molecule type: protein
 A;Residues: 154-163 <MOD>
 R;Carraway, R.E.; Mitra, S.P.
 Biochem. Biophys. Res. Commun. 179, 301-308, 1991.
 A;Title: Purification of large neuropeptidyl-like decapeptide from canine intestine and its identifi
 A;Reference number: JN0293; MUID:91354266; PMID:188359
 A;Accession: JN0293
 A;Molecule type: protein
 A;Residues: 24-43 <CARS>
 A;Experimental source: small intestine
 R;Carraway, R.E.; Mitra, S.P.
 J. Biol. Chem. 265, 8627-8631, 1990
 A;Title: Differential processing of neuropeptidyl-like decapeptides from canine brain
 A;Reference number: A36272; MUID:90256983; PMID:2341398
 A;Accession: A36272
 A;Molecule type: protein
 A;Residues: 128-147 <CA2>
 C;Superfamily: neurotensin
 C;Keywords: hormone; neuropeptide; pyroglutamatic acid
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-148/Product: large neuropeptidyl N-125 #status experimental <LM>
 F;143-148/Product: neuropeptidyl N #status experimental <NNM>
 F;151-163/Product: neuropeptidyl N #status experimental <NTS>
 F;151/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experime
 Query Match 84.8%; Score 28; DB 1; Length 170;
 Best Local Similarity 71.4%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 157 PRRPyVL 163

RESULT 32
 A10432
 probable stringent starvation protein B sspB [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Accession: A10432
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 12-Jul-2004
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 Il, M.; Rutherford, K.; Simmonds, M.; Selton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:1586360
 A;Accession: A10432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-171 <KUR>
 A;Cross-references: UNIPROT:Q8ZB64; GB:AL590842; PIDN:CAC92789_1; PID:915981482; GSPDB:G
 C;Geneticloc:
 C;Gene: sspB
 C;Superfamily: ClpX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 171;
 Best Local Similarity 71.4%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 8 PRRPyVL 14

RESULT 33
 F87546
 transcription regulator, AraC family [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;accession: F87260
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
 B.; Laub, M.T.; Devoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay,
 N.; J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. NATL. Acad. SCI. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; NID:21173698; PMID:11259647
 A;Accession: F87246
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9A5P8; GB:AE005673; PIDN:AAK24370.1; GSPDB:GN
 C;Genetics: CC2399

RESULT 34

F87260 WebB/TacR/CpxP family protein [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: F87260
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
 B.; Laub, M.T.; Devoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay,
 N.; J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. NATL. Acad. SCI. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; NID:21173698; PMID:11259647
 A;Accession: F87260
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-316 <STO>
 A;Cross-references: UNIPROT:Q9ABX5; GB:AE005673; PIDN:AAK22082.1; GSPDB:GN
 C;Genetics: CC0095

Query Match Score 28; DB 2; Length 312;
 Best Local Similarity 57.1%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRDYXL 8
 Db 108 PARYT1 114

RESULT 35

T03612 chalcone synthase homolog - rice
 C;Species: Oryza sativa (rice)
 C;Accession: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 15-Mar-2004
 C;Accession: T03612
 R;Zhang, Y.; Ou, L.; Xie, M.; Gu, H.; Chen, Z.
 A;Description: cDNA sequence of a CHS-like gene from rice flower.
 A;Accession: T03612
 A;Reference number: Z14978
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-389 <ZHA>
 A;Cross-references: EMBL:X01811; NID:91008983; PID:91008984
 A;Experimental source: cv. Zhonghua 10
 C;Genetics:
 A;Gene: chs1k
 C;Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PDRPyDL 215

RESULT 36

T02970 hypothetical protein YW2 - rice
 C;Species: Oryza sativa (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02970
 R.Hihara, Y.; Hara, C.; Uchimura, H.
 Plant Mol. Biol. 30, 1181-1193, 1996
 A;Title: Isolation and characterization of two cDNA clones for mRNAs that are abundantly
 A;Experimental source: anther, cultivar Hayayuki
 C;Superfamily: Type III polyketide synthase
 A;Accession: T02970
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-389 <HIN>
 A;Cross-references: UNIPROT:023811; EMBL:D50576; NID:92645169; PIDN:BAA23618_1; PID:9264
 A;Reference number: Z14800; MUID:96311007; PMID:8704128

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PDRPyDL 215

RESULT 37

T10742 chalcone synthase homolog Chs1 - Monterey pine
 C;Species: Pinus radiata (Monterey pine)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Mar-2004
 C;Accession: T10742
 R.Walden, A.R.; Walter, C.; Gardner, R.C.
 submitted to the EMBL Data Library, February 1997
 A;Description: Genes expressed in pinus radiata male cones.
 A;Reference number: Z17111
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-390 <WAL>
 A;Cross-references: EMBL:U90341; NID:92507616; PID:92507617
 A;Experimental source: strain 880/607; tissue_type male cone; clone PAW192
 C;Superfamily: Type III polyketide synthase
 Query Match 84.8%; Score 28; DB 2; Length 390;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PERPYDL 215

RESULT 38

T06585 ammonium transporter 2 - tomato
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06585
 R.Lauter, F.R.; Nurnmann, O.; Frommer, W.B.
 submitted to the EMBL Data Library, January 1996
 A;Description: Cloning and characterization of the ammonium transporter LeAMT2 from toma
 A;Reference number: Z15776

Query Match 84.8%; Score 28; DB 2; Length 514;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 409 PNRPYGL 415

RESULT 39

S75169 urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
 N;Alternate names: protein Sll1750
 C;Species: Synechocystis sp.

A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S75169
 R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanebe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S75169
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-569 <KAN>
 A;Cross-references: UNIPROT:P773061; EMBL:D90903; GB:AB001339; NID:91652127; PIDN:BAA1708;
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Gene: ureC
 C;Superfamily: urease, alpha subunit; urease 62k chain homology
 C;Keywords: hydrolase; metalloprotein; nickel
 P5-552;Domain: urease 62k chain homology <U62>
 P,136,138,219,362/Binding site: nickel 2 (His, His, Lys, ASP) #status predicted
 Query Match 84.8%; Score 28; DB 2; Length 569;
 Best Local Similarity 57.1%; Pred. No. 2.1e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 302 PTRPYTI 308

RESULT 40

C16950 uracil (EC 3.5.1.5) 6'k chain - Bacillus sp. (strain TB-90)
 N;Alternate names: urc protein
 C;Species: Bacillus sp.

C;Accession: C16950
 R.Maeda, M.; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
 J. Bacteriol. 176, 433-442, 1994
 A;Title: Cloning, sequencing, and expression of thermostable Bacillus sp. strain TB-90 ur
 A;Reference number: A16950; MUID:94117379; PMID:8288539
 A;Accession: C16950
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-569 <MAE>
 A;Cross-references: UNIPROT:Q07397; GB:D14439; NID:9393296; PIDN:BAA03325_1; PID:9216362
 C;Superfamily: Urease, alpha subunit; uracil 62k chain homology
 C;Keywords: hydrolase,

F,5-552/Domain: urease 62K chain homology <U62>

Query Match 84.8%; Score 28; DB 2; Length 569;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0;
Gaps 0;

Qy 2 PXRPYXL 8
Db 302 PTRPYTI 308
| ||| :

Search completed: March 28, 2005, 08:38:06
Job time : 42 secs

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GenCore version 5.1.6
(Without alignments)

57.583 Million cell updates/sec

Om protein - protein search, using sw model

Run on:

March 28, 2005, 08:33:43 ; Search time 46 Seconds

(Without alignments)

57.583 Million cell updates/sec

Title: US-10-036-918B-4

Perfect score: 33

Sequence: 1 XPXRPyXL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 33110923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100% summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/us07_pubcomb.pep:*

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4: /cgn2_6/ptodata/2/pubpaa/us06_pubcomb.pep:*

5: /cgn2_6/ptodata/2/pubpaa/us07_NEWPUB.PEP:*

6: /cgn2_6/ptodata/2/pubpaa/PCTRS_PUBCOMB.PEP:*

7: /cgn2_6/ptodata/2/pubpaa/us07_pub_comb.pep:*

8: /cgn2_6/ptodata/2/pubpaa/us08_pubcomb.pep:*

9: /cgn2_6/ptodata/2/pubpaa/us10C_pubcomb.pep:*

10: /cgn2_6/ptodata/2/pubpaa/us09B_pubcomb.pep:*

11: /cgn2_6/ptodata/2/pubpaa/us09C_pubcomb.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/us11_NEWPUB.PEP:*

19: /cgn2_6/ptodata/2/pubpaa/us60_NEWPUB.PEP:*

20: /cgn2_6/ptodata/2/pubpaa/us60_pubcomb.pep:*

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	29	87.9	65	15 US-10-437-963-110356	Sequence 110356,
2	29	87.9	78	15 US-10-424-599-232759	Sequence 232759,
3	29	87.9	129	15 US-10-424-599-25746	Sequence 25746,
4	29	87.9	157	15 US-10-094-749-2431	Sequence 2431, App
5	29	87.9	216	9 US-09-863-200-4	Sequence 4, Appli
6	29	87.9	216	15 US-10-407-079-106	Sequence 106, App
7	29	87.9	247	15 US-10-424-599-201130	Sequence 201130,
8	29	87.9	281	15 US-10-283-122A-72786	Sequence 72786, A
9	29	87.9	312	15 US-10-283-122A-54324	Sequence 54324, A
10	29	87.9	315	9 US-09-815-242-11014	Sequence 11014, A
11	29	87.9	315	15 US-10-283-122A-58158	Sequence 58158, A
12	29	87.9	315	15 US-10-283-122A-67564	Sequence 67564, A
13	29	87.9	316	9 US-09-815-242-11934	Sequence 11934, A

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	29	87.9	65	15 US-10-437-963-110356	Sequence 110356,
2	29	87.9	78	15 US-10-424-599-232759	Sequence 232759,
3	29	87.9	129	15 US-10-424-599-25746	Sequence 25746,
4	29	87.9	157	15 US-10-094-749-2431	Sequence 2431, App
5	29	87.9	216	9 US-09-863-200-4	Sequence 4, Appli
6	29	87.9	216	15 US-10-407-079-106	Sequence 106, App
7	29	87.9	247	15 US-10-424-599-201130	Sequence 201130,
8	29	87.9	281	15 US-10-283-122A-72786	Sequence 72786, A
9	29	87.9	312	15 US-10-283-122A-54324	Sequence 54324, A
10	29	87.9	315	9 US-09-815-242-11014	Sequence 11014, A
11	29	87.9	315	15 US-10-283-122A-58158	Sequence 58158, A
12	29	87.9	315	15 US-10-283-122A-67564	Sequence 67564, A
13	29	87.9	316	9 US-09-815-242-11934	Sequence 11934, A

Result No.	Score	Query	Match Length	DB ID	Description
1	29	87.9	65	15 US-10-437-963-110356	Sequence 65153, A
2	29	87.9	78	15 US-10-424-599-232759	Sequence 65958, A
3	29	87.9	129	15 US-10-424-599-25746	Sequence 70335, A
4	29	87.9	157	9 US-09-815-242-10048	Sequence 1048, A
5	29	87.9	216	9 US-09-815-242-13897	Sequence 13897, A
6	29	87.9	216	15 US-10-282-122A-43192	Sequence 43192, A
7	29	87.9	216	15 US-10-282-122A-55333	Sequence 55833, A
8	29	87.9	216	15 US-10-282-122A-5906	Sequence 5606, A
9	29	87.9	216	15 US-10-282-122A-65880	Sequence 6080, A
10	29	87.9	216	15 US-10-282-122A-68169	Sequence 6894, A
11	29	87.9	216	15 US-10-282-122A-75393	Sequence 65569, A
12	29	87.9	216	15 US-10-282-122A-75293	Sequence 75293, A
13	29	87.9	216	15 US-10-282-122A-76171	Sequence 76171, A
14	29	87.9	216	15 US-10-282-122A-77112	Sequence 77112, A
15	29	87.9	216	15 US-10-282-122A-77771	Sequence 77771, A
16	29	87.9	216	15 US-10-424-599-21526	Sequence 21526,
17	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
18	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
19	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
20	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
21	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
22	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
23	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
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26	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
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40	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
41	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
42	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
43	29	87.9	216	15 US-10-424-599-145135	Sequence 145135,
44	28	87.9	216	8 US-09-863-011A-8	Sequence 13950, A
45	28	87.9	216	8 US-10-634-033-B	Sequence 70896, A
46	28	84.8	8	10 US-09-911-277A-8	Sequence 52874,
47	28	84.8	8	10 US-09-717-332A-8	Sequence 15135,
48	28	84.8	8	10 US-09-757-333D-8	Sequence 149403,
49	28	84.8	8	10 US-09-918-722A-8	Sequence 20, App
50	28	84.8	8	14 US-10-071-779-8	Sequence 8, Appli
51	28	84.8	8	16 US-10-634-033-B	Sequence 8, Appli
52	28	84.8	8	17 US-10-835-257-B	Sequence 8, Appli
53	28	84.8	8	13 9 US-09-985-672-2	Sequence 8, Appli
54	28	84.8	8	13 10 US-09-988-793-4	Sequence 8, Appli
55	28	84.8	8	13 14 US-10-050-200-21	Sequence 21, Appli
56	28	84.8	8	13 14 US-10-424-599-145135	Sequence 1, Appli
57	28	84.8	8	13 15 US-10-188-697-1	Sequence 1, Appli
58	28	84.8	8	13 15 US-10-655-516-8	Sequence 8, Appli
59	28	84.8	8	13 15 US-10-157-621-66	Sequence 66, Appli
60	28	84.8	8	13 15 US-10-177-701-11A-1	Sequence 14, Appli
61	28	84.8	8	13 17 US-10-839-017-4	Sequence 4, Appli
62	28	84.8	8	15 16 US-10-424-599-132088	Sequence 132088,
63	28	84.8	8	16 15 US-10-424-599-169226	Sequence 169226,
64	28	84.8	8	16 15 US-10-424-599-176554	Sequence 176654,
65	28	84.8	8	16 15 US-10-424-599-201773	Sequence 5773, A
66	28	84.8	8	16 15 US-09-741-669-350	Sequence 35, App
67	28	84.8	169	11 US-09-927-565A-3	Sequence 3, Appli
68	28	84.8	169	11 US-09-927-565A-4	Sequence 4, Appli
69	28	84.8	170	14 US-09-927-565A-1	Sequence 1, Appli
70	28	84.8	170	14 US-10-241-220-111	Sequence 111, App
71	28	84.8	170	14 US-10-241-220-111	Sequence 316, App
72	28	84.8	170	15 US-10-235-022-316	Sequence 202335,
73	28	84.8	170	15 US-10-427-963-115140	Sequence 115140,
74	28	84.8	170	15 US-10-427-963-115140	Sequence 6, Appli
75	28	84.8	170	15 US-09-828-378-6	Sequence 7, Appli
76	28	84.8	170	15 US-10-427-963-103558	Sequence 13658,
77	28	84.8	170	15 US-09-828-378-2	Sequence 2, Appli
78	28	84.8	170	15 US-10-427-963-165801	Sequence 165801,
79	28	84.8	170	15 US-10-427-963-200465	Sequence 200465,
80	28	84.8	170	15 US-10-427-963-200465	Sequence 148518,
81	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A
82	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A
83	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A
84	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A
85	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A
86	28	84.8	170	14 US-10-156-761-11122	Sequence 11122, A

RESULT 1
US-10-437-963-110356
; Sequence 110356, Application US/10437963
; Publication No. US20040223343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Jing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5221)B
CURRENT APPLICATION NUMBER: US/10/437-963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 110356.
LENGTH: 65
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14427C.1.pep
US-10-437-963-110356

Query Match 87.9%; Score 29; DB 16; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 28 84.8 2142 16 US-10-437-963-180052
Qy 2 PXRPYXL 8
Db 40 PIRPYSL 46

ALIGNMENTS

RESULT 3
US-10-424-599-257546
; Sequence 257546, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plant and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 257546
LENGTH: 129
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_74589C.1.pep
US-10-424-599-257546

Query Match 87.9%; Score 29; DB 15; Length 129;
Best Local Similarity 71.4%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 28 84.8 34 PTPYDYL 40

RESULT 4
US-10-094-749-2431
; Sequence 2431, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TENSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: ITIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOKIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3181
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2431
 ; LENGTH: 157
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-094-749-2431.

 Query Match 87.9%; Score 29; DB 15; Length 157;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
 Matches 5; Other Information: Qy 2 PXRPyXL 8 Db 43 PNRPyTL 49

 RESULT 5
 US-09-863-200-4
 ; Sequence 4, Application US/09863200
 ; Publication No. US20020039762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc
 ; TITLE OF INVENTION: 26908 NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 38155-20014.00
 ; CURRENT APPLICATION NUMBER: US/09/863,200
 ; CURRENT FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/206,019
 ; PRIOR FILING DATE: 2000-05-22
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 216
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Other Information: Qy 191 PDRPySL 197 Db 191 PDRPySL 197

 RESULT 6
 US-10-407-079-106
 ; Sequence 4, Application US/09863200
 ; Publication No. US20020039762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Silos-Santiso, Immaculada
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Galvin, Katherine M.
 ; TITLE OF INVENTION: 45449, 50289, 52872 AND 26908 MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: WO2003-05109NIM
 ; CURRENT APPLICATION NUMBER: US/10/407,079
 ; CURRENT FILING DATE: 2003-04-03

 RESULT 6
 US-10-407-079-106
 ; Sequence 106, Application US/10407079
 ; Publication No. US20030215860A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Silos-Santiso, Immaculada
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Galvin, Katherine M.
 ; TITLE OF INVENTION: 18636, 2466, 43238, 1983, 52881, 2398, Best Local Similarity 71.4%; Pred. No. 5e+02; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
 ; Other Information: Current Application Number: US/10/407,079
 ; Current Filing Date: 2003-04-03

 Query Match 87.9%; Score 29; DB 15; Length 216;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
 Matches 5; Other Information: Qy 2 PXRPyXL 8 Db 191 PDRPySL 197

 RESULT 7
 US-10-424-599-201130
 ; Sequence 201130, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-03-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 201130
 ; LENGTH: 247
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Glycine max
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(247)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Other Information: Qy 2 PXRPyXL 8 Db 191 PDRPySL 197

 Query Match 87.9%; Score 29; DB 15; Length 247;
 Best Local Similarity 71.4%; Pred. No. 5e+02; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
 Matches 5; Other Information: Other Information: Qy 2 PXRPyXL 8 Db 191 PDRPySL 197

```

Db      80 PARPYFL 86
; Publication No. US20040029129A1
; GENERAL INFORMATION;
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72785
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; LOCATION: (103).-(103)
; OTHER INFORMATION: X=x any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (256)..(256)
; OTHER INFORMATION: X=x any amino acid
US-10-282-122A-72786
Query Match          87.9%; Score 29; DB 15; Length 281;
Best Local Similarity 71.4%; Pred. No. 5.7e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 PXRPyXL 8
Db      60 PARPYFL 66
; Publication No. US20040029129A1
; GENERAL INFORMATION;
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
RESULT 9
US-10-282-122A-54324
; Sequence 54324, Application US/10282122A

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Db | ||| |
 67 PKRPyTL 73

RESULT 13
 Sequence 11934, Application US/09815242
 Patent No. US2000061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 Prokaryotes
 FILE REFERENCE: ELTRA-011A
 CURRENT APPLICATION NUMBER: US/09/815, 242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269, 308
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 66513
 LENGTH: 316
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66513
 Query Match 87.9%; Score 29; DB 9; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPYXL 8
 Db 67 PKRPyTL 73

RESULT 14
 US-10-282-122A-66513
 Sequence 66958, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zanudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTRA-034A
 CURRENT APPLICATION NUMBER: US/10/282, 122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625

CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR APPLICATION NUMBER: 60/242, 577
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 66513
 LENGTH: 316
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66513
 Query Match 87.9%; Score 29; DB 15; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PROR FILING DATE: 2000-11-27
; PROR APPLICATION NUMBER: 60/257,931
; PROR FILING DATE: 2000-12-22
; PROR APPLICATION NUMBER: 60/267,636
; PROR FILING DATE: 2001-02-09
; PROR APPLICATION NUMBER: 60/269,308
; PROR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66958
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Pasteurella multocida

US-10-282-122A-66958

Query Match 87.9%; Score 29; DB 15; Length 317;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 2;

Qy	2 PXRPyXL 8
Db	68 PRPryTL 74

RESULT 16

US-10-282-122A-70135

; Sequence 70135, Application US/10282122A
; Publication No. US2004020029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Lianggu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haebelbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA_034A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/205,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10048

LENGTH: 319

TYPE: PRT

ORGANISM: Escherichia coli

US-09-815-242-10048

Query Match 87.9%; Score 29; DB 9; Length 319;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 2;

Qy	2 PXRPyXL 8
Db	70 PQRPYTL 76

RESULT 18

US-09-815-242-13897

; Sequence 13897, Application US/09815242

; Patent No. US2002001569A1

; GENERAL INFORMATION:

APPLICANT: Haebelbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 707614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 70135

LENGTH: 317

TYPE: PRT

ORGANISM: Pseudomonas syringae

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 FILE REFERENCE: ELITRA_011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 13897
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Salmonella typhi
 US-09-815-242-13897
 Query Match 87.9%; Score 29; DB 9; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Identity 2 PYRPyXL 8
 % 70 PORPyYL 76
 RESULT 19
 US-10-282-122A-43192
 Sequence 43192, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Karl
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: SeqIn version 3.1
 SEQ ID NO 55833
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Enterobacter cloacae
 US-10-282-122A-55833
 Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 21
 US-10-282-122A-59606
 ; Sequence 59606, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; CURRENT APPLICATION NUMBER: 60/191,078
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; SEQ ID NO: 59606
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 ; US-10-282-122A-65080
 ; Query Match 87.9%; Score 29; DB 15; Length 319;
 ; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Mismatches 2; Indels 0; Gaps 0;
 ; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 22
 US-10-282-122A-65080
 ; Sequence 65080, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A

RESULT 23
 US-10-282-122A-65084
 ; Sequence 65084, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A

RESULT 24
 US-10-282-122A-65084
 ; Sequence 65084, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu

CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68594
; LENGTH: 319
; TYPE: PRT
; ORGANISM: *Neisseria meningitidis*
; US-10-282-122A-68594
; Query Match 87.9%; Score 29; DB 15; Length 319;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02;
; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 2 PXRPYXL 8
; Db 67 PRPYPYL 73
; LENGTH: 319
; TYPE: PRT
; ORGANISM: *Proteus mirabilis*
; US-10-282-122A-68569
; Query Match 87.9%; Score 29; DB 15; Length 319;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02;
; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 2 PXRPYXL 8
; Db 70 PRPYPYL 76
; LENGTH: 319
; TYPE: PRT
; ORGANISM: *Salmonella typhimurium*
; US-10-282-122A-75293
; Sequence 75293, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianggu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheeyl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75293
; LENGTH: 319
; TYPE: PRT
; ORGANISM: *Salmonella typhimurium*

US-10-282-122A-75293

Publication No. US20040029129A1
 GENERAL INFORMATION:
 Sequence 76171, Application US/10282122A

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 70 PQRPYTL 76

RESULT 26

US-10-282-122A-76171
 Sequence 76171, Application US/10282122A
 Publication No. US20040029129A1

GENERAL INFORMATION:
 Sequence 76171, Application US/10282122A

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl
 APPLICANT: Ohlen, Kari

APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Judith

APPLICANT: Olsen, Kari
 APPLICANT: Wall, Daniel

APPLICANT: Trawick, John
 APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

APPLICANT: Forayth, R.

APPLICANT: Xu, H.

APPLICANT: Identification of Essential Genes in Microorganisms

CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/277,931
 PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/277,931
 PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 77412
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Vibrio cholerae

US-10-282-122A-77412

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 70 PQRPYTL 76

RESULT 28

US-10-282-122A-77971
 Sequence 77971, Application US/10282122A
 Publication No. US20040029129A1

GENERAL INFORMATION:
 Sequence 77971, Application US/10282122A

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl
 APPLICANT: Ohlen, Kari

APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Judith

APPLICANT: Olsen, Kari
 APPLICANT: Wall, Daniel

APPLICANT: Trawick, John
 APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

APPLICANT: Forayth, R.

APPLICANT: Xu, H.

ORGANISM: Salmonella typhi

US-10-282-122A-76171

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 70 PQRPYTL 76

RESULT 27

US-10-282-122A-77412
 Sequence 77412, Application US/10282122A

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 6/0/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 6/0/206,,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 6/0/207,,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 6/0/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 6/0/230,,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 6/0/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 6/0/253,,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 6/0/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 6/0/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 6/0/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77971
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Yersinia pestis
; US-10-282-122A-77971
;
Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0;
Qy 2 PXPYXXL 8
Db 70 PRRPYTL 76
RESULT 29
US-10-282-122A-68469
Sequence 68469, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 6/0/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 6/0/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 6/0/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 6/0/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 6/0/230,,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 6/0/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 6/0/253,,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 6/0/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 6/0/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 6/0/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68469
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-10-282-122A-68469
; Software: PatentIn version 3.1
; SEQ ID NO 77971
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Yersinia pestis
; US-10-282-122A-51090
; Sequence 51090, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 6/0/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 6/0/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 6/0/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 6/0/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 6/0/230,,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 6/0/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 6/0/253,,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 6/0/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 6/0/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 6/0/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51090

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;
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Bordetella pertussis
; US-10-282-122A-51090

Query Match      Best Local Similarity 87.9%; Score 29; DB 15; Length 321;
Matches          5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy               2 PXRPYXL 8
Db               67 PQRPYTL 73

RESULT 31
US-10-282-122A-47697
Sequence 47697, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/270,581
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50581
LENGTH: 323
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50581

RESULT 32
US-10-282-122A-50581
Sequence 215226, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou Yiliua
APPLICANT: Cao Yongwei
APPLICANT: Title of Invention: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

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NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215226
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36374C.1.pep
US-10-424-599-215226

Query Match 87.9%; Score 29; DB 15; Length 331;
Best Local Similarity 71.4%; Pred. No. 6.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 293 PSRPyYL 299

RESULT 34
US-10-437-963-145135
; Sequence 145135, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 145135
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45883C.1.pep
US-10-437-963-145135

Query Match 87.9%; Score 29; DB 16; Length 392;
Best Local Similarity 71.4%; Pred. No. 7.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 364 PTpRPyQL 370

RESULT 35
US-10-278-141-4
; Sequence 4, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LIU, Duying Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOURY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Damniel B.
; APPLICANT: VUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096.PCT
; CURRENT APPLICATION NUMBER: US/10/296, 081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205, 628; 60/206, 222; 60/207, 566; 60/208, 834; 60/209, 834; 60/208, 861
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/205, 628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208, 861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US/10/278, 141
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/208, 834
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/207, 566
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US/11/16285
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205, 628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208, 861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/206, 222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030138818A1 1258785CD1
US-10-278-141-4

Query Match 87.9%; Score 29; DB 14; Length 432;
Best Local Similarity 71.4%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 393 PDpRySL 399

RESULT 36
US-10-296-091-4
; Sequence 4, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LIU, Duying Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOURY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Damniel B.
; APPLICANT: VUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096.PCT
; CURRENT APPLICATION NUMBER: US/10/296, 081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205, 628; 60/206, 222; 60/207, 566; 60/208, 834; 60/209, 834; 60/208, 861
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
; SOFTWARE: PERL Program
; SEQ ID NO 4

Db 411 PDRPYSL 417

LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc feature

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030220477A1 1258785CD1
US-10-296-081-4

RESULT 37
US-10-400-991-20
; Sequence 20, Application US/104000991
; Publication No. US20030224417A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Weitch, Nadine S.
; APPLICANT: Hunter, John J.
; APPLICANT: White, David
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chun, Myoung
TITLE OF INVENTION: 14400, 2838, 14618, 15334, 14274, 32164, 32705, 23224,
TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN TRANSMEMBRANE
TITLE OF INVENTION: PROTEIN-PROTEIN COUPLES RECEPTORS
FILE REFERENCE: MP03-0240MNIM

CURRENT APPLICATION NUMBER: US/10/400,991
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US/10/190,469

PRIOR FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US/09/439,159

PRIOR APPLICATION NUMBER: US/09/137,063
PRIOR FILING DATE: 1998-08-20

PRIOR APPLICATION NUMBER: US/10/167,192
PRIOR FILING DATE: 2002-06-11

PRIOR APPLICATION NUMBER: US/09/420,187
PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US/09/173,869
PRIOR FILING DATE: 1998-10-16

PRIOR APPLICATION NUMBER: US/10/339,056
PRIOR FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US/09/377,429
PRIOR FILING DATE: 1999-08-19

PRIOR APPLICATION NUMBER: US/09/135,726
PRIOR FILING DATE: 1998-08-19

PRIOR APPLICATION NUMBER: US/09/911,583
PRIOR FILING DATE: 2001-07-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450

TYPE: PRT
ORGANISM: Homo Sapiens

Query Match 87.9%; Score 29; DB 15; Length 450;
Best Local Similarity 71.4%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-10-400-991-20

RESULT 38
US-10-156-761-13950
; Sequence 13950, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HONIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAO
; APPLICANT: SAKAKI, YOSHIO
; APPLICANT: HATTORI, MASAHIRI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02

SEQ ID NO 13950
LENGTH: 455

TYPE: PRT
ORGANISM: Streptomyces avermitilis

US-10-156-761-13950

Query Match 87.9%; Score 29; DB 14; Length 455;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
Db 393 PDRPYSL 399

RESULT 39
US-10-425-114-70896
; Sequence 70896, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B

CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70896
LENGTH: 569

TYPE: PRT
ORGANISM: Zea mays
FEATURE: OTHER INFORMATION: Clone ID: LIB3150-018-B2_FLI.pep

US-10-425-114-70896

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
Db 157 PSRPYVL 163

RESULT 40
US-10-425-114-51274
; Sequence 51274, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screeen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51274
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-094-A6_FLI.pep
; US-10-425-114-51274

Query Match 87.9%; Score 29; DB 15; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPAPYXL 8
Db 154 PSRPPYL 160

Search completed: March 28, 2005, 08:39:57
Job time : 47 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: March 28, 2005, 08:33:43 ; Search time 44 Seconds
(without alignments)
13.573 Million cell updates/sec

Title: US-10-036-918B-4

Perfect score: 33

Sequence: 1XPXRPyXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents Aa:*

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4: /cgn2_6/pctodata/1/iaa/6B-COMB.pep:*

5: /cgn2_6/pctodata/1/iaa/6C-COMB.pep:*

6: /cgn2_6/pctodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description	
1	30	90.9	1100	1	US-08-357-598-11	Sequence 11, Appli	
2	30	90.9	1100	2	US-09-003-289-11	Sequence 11, Appli	
3	30	90.9	1100	5	PCT-US95-16435-11	Sequence 11, Appli	
4	29	87.9	323	4	US-09-543-6625	Sequence 6625, Appli	
5	29	87.9	323	4	US-09-489-039A-12281	Sequence 12281, Appli	
6	29	87.9	328	4	US-09-543-681A-4495	Sequence 4495, Appli	
7	29	87.9	332	4	US-09-252-991A-21222	Sequence 21222, Appli	
8	29	87.9	1098	3	US-08-946-994-17	Sequence 17, Appli	
9	29	87.9	1099	3	US-08-665-574C-16	Sequence 16, Appli	
10	29	87.9	1912	4	US-09-949-016-0490	Sequence 10490, Appli	
11	28	84.8	7	4	US-09-528-200-179	Sequence 179, Appli	
12	28	84.8	8	3	US-09-484-318-7	Sequence 7, Appli	
13	28	84.8	8	3	US-09-484-319-7	Sequence 7, Appli	
14	28	84.8	8	3	US-09-484-320-7	Sequence 7, Appli	
15	28	84.8	8	3	US-09-484-321-7	Sequence 7, Appli	
16	28	84.8	8	3	US-09-484-323-7	Sequence 7, Appli	
17	28	84.8	8	3	US-09-528-769-8	Sequence 7, Appli	
18	28	84.8	8	3	US-09-636-170-7	Sequence 7, Appli	
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20	28	84.8	8	4	US-09-528-200-178	Sequence 178, Appli	
21	28	84.8	8	4	US-09-863-971A-8	Sequence 8, Appli	
22	28	84.8	8	4	US-09-864-011A-8	Sequence 8, Appli	
23	28	84.8	8	4	US-09-978-725A-8	Sequence 8, Appli	
24	28	84.8	9	4	US-09-528-200-177	Sequence 177, Appli	
25	28	84.8	10	4	US-09-522-200-194	Sequence 194, Appli	
26	28	84.8	12	1	US-08-141-324-6	Sequence 6, Appli	
27	28	84.8	12	1	US-08-541-902-6	Sequence 6, Appli	
28	84.8	12	3	US-09-202-832-4	Sequence 4, Appli		
29	84.8	13	1	US-07-714-540-8	Sequence 8, Appli		
30	84.8	13	2	US-08-747-137-117	Sequence 11, Appli		
31	84.8	13	2	US-08-737-299A-1	Sequence 1, Appli		
32	84.8	13	3	US-08-334-254A-1	Sequence 8, Appli		
33	84.8	13	3	US-08-609-534-8	Sequence 8, Appli		
34	84.8	13	4	US-09-289-693-1	Sequence 10, Appli		
35	84.8	13	3	US-09-355-869-2	Sequence 161, Appli		
36	84.8	13	3	US-09-605-990-8	Sequence 162, Appli		
37	84.8	13	3	US-09-420-797B-8	Sequence 8, Appli		
38	84.8	13	4	US-09-605-991-1	Sequence 1, Appli		
39	84.8	13	4	US-09-609-534-8	Sequence 8, Appli		
40	84.8	13	4	US-09-528-200-10	Sequence 15, Appli		
41	84.8	13	4	US-09-528-200-161	Sequence 13714, Appli		
42	84.8	13	4	US-09-528-200-162	Sequence 16005, Appli		
43	84.8	13	4	US-09-248-796A-16074	Sequence 16074, Appli		
44	84.8	13	4	US-09-252-991A-29303	Sequence 29303, Appli		
45	84.8	13	4	US-09-252-991A-15237	Sequence 15237, Appli		
46	84.8	134	5	PCT-US93-07213-15	Sequence 16073, Appli		
47	84.8	165	4	US-09-489-039A-13714	Sequence 10807, Appli		
48	84.8	169	3	US-09-002-114-4	Sequence 16005, Appli		
49	84.8	169	3	US-09-02-114-1	Sequence 16074, Appli		
50	84.8	170	3	US-09-270-767-37831	Sequence 1673, Appli		
51	84.8	171	4	US-09-949-016-7377	Sequence 7377, Appli		
52	84.8	185	4	US-09-248-796A-16073	Sequence 9510, Appli		
53	84.8	231	4	US-09-902-540-10807	Sequence 10807, Appli		
54	84.8	240	4	US-09-540-16005	Sequence 16005, Appli		
55	84.8	281	4	US-09-248-796A-16074	Sequence 16074, Appli		
56	84.8	317	4	US-09-252-991A-29303	Sequence 29303, Appli		
57	84.8	322	4	US-09-901-540-15237	Sequence 15237, Appli		
58	84.8	567	4	US-09-328-352-5912	Sequence 5912, Appli		
59	84.8	568	1	US-07-732-242C-3	Sequence 10005, Appli		
60	84.8	1279	4	US-09-248-796A-16074	Sequence 16005, Appli		
61	84.8	1279	4	US-09-364-425B-58	Sequence 16074, Appli		
62	84.8	169	4	US-09-270-767-37831	Sequence 1673, Appli		
63	84.8	169	4	US-09-946-993-123-4	Sequence 53031, Appli		
64	84.8	27	81.8	551	4	US-09-489-039A-9510	Sequence 9510, Appli
65	84.8	27	81.8	3	US-09-129-075-4	Sequence 4, Appli	
66	84.8	27	81.8	3	US-09-346-237-3	Sequence 3, Appli	
67	84.8	27	81.8	726	3	US-09-931-858B-169	Sequence 13, Appli
68	84.8	27	81.8	4	US-09-544-123-4	Sequence 4, Appli	
69	84.8	27	81.8	915	3	US-09-346-237-2	Sequence 4, Appli
70	84.8	20	81.8	3	US-09-605-999A-314	Sequence 314, Appli	
71	84.8	26	78.8	4	US-09-500-124-314	Sequence 43, Appli	
72	84.8	46	78.8	4	US-09-640-737-43	Sequence 32041, Appli	
73	84.8	100	4	US-09-250-991A-32041	Sequence 27, Appli		
74	84.8	105	1	US-09-482-577B-27	Sequence 47, Appli		
75	84.8	105	3	US-09-482-577B-27	Sequence 22, Appli		
76	84.8	105	3	US-09-289-222B-31	Sequence 31, Appli		
77	84.8	105	3	US-09-218-176-10	Sequence 10, Appli		
78	84.8	105	3	US-09-345-237-3	Sequence 31, Appli		
79	84.8	105	3	US-09-931-858B-169	Sequence 169, Appli		
80	84.8	105	3	US-09-981-739-169	Sequence 169, Appli		
81	84.8	105	4	US-09-128-026-169	Sequence 169, Appli		
82	84.8	105	4	US-09-496-398-22	Sequence 22, Appli		
83	84.8	105	4	US-09-220-616-169	Sequence 169, Appli		
84	84.8	105	4	US-09-374-958C-61	Sequence 61, Appli		
85	84.8	105	4	US-09-220-527-169	Sequence 169, Appli		
86	84.8	105	4	US-09-220-407-169	Sequence 169, Appli		
87	84.8	106	4	US-09-278-238-36	Sequence 36, Appli		
88	84.8	106	4	US-09-248-796A-15619	Sequence 15619, Appli		
89	84.8	107	4	US-09-543-681A-8265	Sequence 8265, Appli		
90	84.8	121	1	US-09-481-377-20	Sequence 20, Appli		
91	84.8	121	2	US-09-491-835-18	Sequence 18, Appli		
92	84.8	121	3	US-09-153-733A-20	Sequence 18, Appli		
93	84.8	121	3	US-09-946-092A-18	Sequence 18, Appli		
94	84.8	121	3	US-09-172-971A-8	Sequence 18, Appli		
95	84.8	121	3	US-09-301-520D-18	Sequence 18, Appli		
96	84.8	121	3	US-09-389-705-20	Sequence 20, Appli		
97	84.8	121	5	PCT-US94-00666-20	Sequence 20, Appli		
98	84.8	121	5	PCT-US94-00665-19	Sequence 18, Appli		
99	84.8	122	1	US-08-458-529B-16	Sequence 16, Appli		
100	84.8	78.8	122	1	US-08-455-559-22	Sequence 22, Appli	

ALIGNMENTS

RESULT 1
US-08-357-598-11
; Sequence 11, Application US/08357598
; Patent No. 5705625
; GENERAL INFORMATION:
; APPLICANT: Civin, Curt I.
; APPLICANT: Small, Donald
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,598
; FILING DATE: 15-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/033001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5099
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; LENGTH: 1100 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5916792 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-357-598-11

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 90.9%; Score 30; DB 1; Length 1100;
Best Local Similarity 71.4%; Pred. No. 4.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
PCT-US95-16435-11
; Sequence 11, Application PC/TUS9516435
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16435
; FILING DATE: 15-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/033001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; LENGTH: 1100 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-16435-11

RESULT 2
US-09-003-289-11
; Sequence 11, Application US/09003289
; Patent No. 5916792
; GENERAL INFORMATION:
; APPLICANT: Civin, Curt I.
; APPLICANT: Small, Donald
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk

Query Match 90.9%; Score 30; DB 5; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 4,3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; N mismatches 2;

Qy	2	PXRPyXL 8
Db	228	PSRPyAL 234

RESULT 4
 US-09-543-681A-6625
 Sequence 6625, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 6625
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-09-543-681A-6625

Query Match 87.9%; Score 29; DB 4; Length 323;
 Best Local Similarity 71.4%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; N mismatches 2;

Qy	2	PXRPyXL 8
Db	74	PLRPYTL 80

RESULT 5
 US-09-489-039A-12281
 Sequence 12281, Application US/09489039A
 Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: GARY BRETON et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12281
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12281

RESULT 6
 US-09-543-681A-4495
 Sequence 4495, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:

RESULT 7
 US-09-252-991A-21222
 Sequence 21222, Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,718
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 21222
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-21222

Query Match 87.9%; Score 29; DB 4; Length 332;
 Best Local Similarity 71.4%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; N mismatches 2;

Qy	2	PXRPyXL 8
Db	83	PKRPyTL 89

RESULT 8
 US-08-946-994-17
 Sequence 17, Application US/08946994
 Patent No. 6210554

GENERAL INFORMATION:
 APPLICANT: Ihle, James N.
 APPLICANT: Silvernointen, Ollie
 APPLICANT: Wittluhn, Bruce A.
 APPLICANT: Quelle, Frederick W.
 TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal Transduction
 TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stearn, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

RESULT 9
 US-09-489-039A-12281

APPLICANT: SEMMLER, WOLFHARD
 APPLICANT: WEIDENMANN, BERTRAM
 APPLICANT: HESSNITS, CARTSEN
 APPLICANT: VOLLMER-ENGERT, RUDOLF
 APPLICANT: SCHNEIDER-MERGNER, JENS
 APPLICANT: BHARGAVA, SARAH
 TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
 TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
 FILE REFERENCE: SCH-1731
 CURRENT APPLICATION NUMBER: US/09/528,200
 CURRENT FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: DE 199 17 713.9
 PRIOR FILING DATE: 1999-09-04
 NUMBER OF SEQ ID NOS: 196
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 179
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: peptide
 US-09-528-200-179

Query Match Best Local Similarity 84.8%; Score 28; DB 4; Length 7;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 1 PRPyYL 7

RESULT 12
 US-09-484-318-7
 ; Sequence 7, Application US/09484318
 ; Patent No. 6180085
 ; GENERAL INFORMATION:
 ; APPLICANT: Achillefu, Samuel
 ; APPLICANT: Rajagopalan, Raghavan
 ; APPLICANT: Dorshow, Richard B
 ; APPLICANT: Bugaj, Joseph E.
 ; TITLE OF INVENTION: NOVEL DYES
 ; FILE REFERENCE: DNA STRING
 ; CURRENT APPLICATION NUMBER: US/09/484,318
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1)
 ; OTHER INFORMATION: THIS IS D-LYSINE.
 ; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 ; OTHER INFORMATION: NEUROTENSIN
 US-09-484-318-7

Query Match Best Local Similarity 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRPyYL 8

RESULT 13
 US-09-484-319-7
 ; Sequence 7, Application US/09484319
 ; Patent No. 6180086

GENERAL INFORMATION:
 APPLICANT: Achillefu, Samuel
 APPLICANT: Rajagopalan, Raghavan
 APPLICANT: Dorshow, Richard B
 APPLICANT: Bugaj, Joseph E.
 TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
 FILE REFERENCE: DNA STRING
 CURRENT APPLICATION NUMBER: US/09/484,319
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: THIS IS D-LYSINE.
 OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 OTHER INFORMATION: NEUROTENSIN
 US-09-484-319-7

Query Match Best Local Similarity 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRPyYL 8

RESULT 15
 US-09-494-321-7
 ; Sequence 7, Application US/09484321
 ; Patent No. 6183726
 ; GENERAL INFORMATION:

APPLICANT: Achilefu, Samuel
 APPLICANT: Rajgopal, Raghavan
 APPLICANT: Dorshaw, Richard B.
 APPLICANT: Bugaj, Joseph E.
 TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
 FILE REFERENCE: 1668-286
 CURRENT APPLICATION NUMBER: US/09/484,321
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 8
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: THIS IS D-LYSINE.
 OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 OTHER INFORMATION: NEUROTENSIN
 ; US-09-484-321-7

Qy	2	PXRPyXL	8	Best Local Similarity	84.8%	Score	28;	DB	3;	Length	8;
Db	2	PRRPyYL	8	Matches	5;	Conservative	0;	Mismatches	+2;	Indels	0;
										Gaps	0;

RESULT 16
 US-09-484-323-7
 Sequence 7, Application US/09484323
 Patent No. 619041
 GENERAL INFORMATION:
 APPLICANT: Achilefu, Samuel
 APPLICANT: Rajgopal, Raghavan
 APPLICANT: Dorshaw, Richard B.
 APPLICANT: Bugaj, Joseph E.
 TITLE OF INVENTION: NOVEL INDOCYANINE DYES
 FILE REFERENCE: DNA STRING
 CURRENT APPLICATION NUMBER: US/09/484,323
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: This is D-lysine.
 OTHER INFORMATION: Description of Artificial Sequence:Analog of
 OTHER INFORMATION: neurotensin.
 ; US-09-484-323-7

Qy	2	PXRPyXL	8	Best Local Similarity	84.8%	Score	28;	DB	3;	Length	8;
Db	2	PRRPyYL	8	Matches	5;	Conservative	0;	Mismatches	+2;	Indels	0;
										Gaps	0;

RESULT 17
 US-09-484-323-7
 Sequence 7, Application US/09484323
 Patent No. 619041
 GENERAL INFORMATION:
 APPLICANT: Achilefu, Samuel
 APPLICANT: Rajgopal, Raghavan
 APPLICANT: Dorshaw, Richard B.
 APPLICANT: Bugaj, Joseph E.
 TITLE OF INVENTION: NOVEL INDOCYANINE DYES
 FILE REFERENCE: DNA STRING
 CURRENT APPLICATION NUMBER: US/09/484,323
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 OTHER INFORMATION: NEUROTENSIN
 ; US-09-484-323-7

Qy	2	PXRPyXL	8	Best Local Similarity	84.8%	Score	28;	DB	3;	Length	8;				
Db	2	PRRPyYL	8											Gaps	0;
										Gaps	0;				

RESULT 18
 US-09-636-170-7
 Sequence 7, Application US/09636170
 Patent No. 6664919
 GENERAL INFORMATION:
 APPLICANT: Achilefu, Samuel
 APPLICANT: Rajgopal, Raghavan
 APPLICANT: Dorshaw, Richard B.
 APPLICANT: Bugaj, Joseph E.
 TITLE OF INVENTION: NOVEL INDOCYANINE DYES
 FILE REFERENCE: DNA STRING
 CURRENT APPLICATION NUMBER: US/09/636,170
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: THIS IS D-LYSINE.
 OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 OTHER INFORMATION: NEUROTENSIN
 ; US-09-636-170-7

Qy	2	PXRPyXL	8	Best Local Similarity	84.8%	Score	28;	DB	3;	Length	8;				
Db	2	PRRPyYL	8											Gaps	0;
										Gaps	0;				

RESULT 19
 US-09-637-518-7
 Sequence 7, Application US/09637518
 Patent No. 621748
 GENERAL INFORMATION:
 APPLICANT: Achilefu, Samuel

Patent No. 6264920
 GENERAL INFORMATION:
 APPLICANT: Achillefu, Samuel I.
 APPLICANT: Rajagopalan, Raghavan
 APPLICANT: Dorschow, Richard B.
 TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
 FILE REFERENCE: dinstrg
 CURRENT APPLICATION NUMBER: US/09/637,518
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1)
 OTHER INFORMATION: THIS IS D-LYSINE.

Query Match 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 5; Conservative 0; Indels 0; Gaps 0; Matches 2; Other Information: Description of Artificial Sequence; ANALOG OF US-09-637-518-7

OY 2 PXRPyXL 8
 Db 2 PRRPyIL 8

RESULT 20
 US-09-228-2000-178
 ; Sequence 178, Application US/09528200
 ; Patent No. 6630570
 ; GENERAL INFORMATION:
 ; APPLICANT: LICHA, KAI
 ; APPLICANT: BECKER, ANDREAS
 ; APPLICANT: SEMMLER, WOLFHARD
 ; APPLICANT: WEIDENMANN, BERTRAM
 ; APPLICANT: HESSNITUS, CARTSEN
 ; APPLICANT: VOLKMER-ENGERT, RUDOLF
 ; APPLICANT: SCHNEIDER-MERGENER, JENS
 ; APPLICANT: BHARGAVA, SARAH
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
 ; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
 ; FILE REFERENCE: SCH-1731
 ; CURRENT APPLICATION NUMBER: US/09/528,200
 ; CURRENT FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9
 ; PRIOR FILING DATE: 1999-09-04
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 178
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence; Synthetic
 ; OTHER INFORMATION: peptide
 ; US-09-528-200-178

Query Match 84.8%; Score 28; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 5; Conservative 0; Indels 0; Gaps 0; Matches 2; Other Information: Description of Artificial Sequence; Synthetic
 ; US-09-528-200-178

Query Match 84.8%; Score 28; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 5; Conservative 0; Indels 0; Gaps 0; Matches 2; Other Information: Xaa at location 1 represents D-Lys. Artificial sequence is completely synthesized.
 ; US-09-863-971A-8

RESULT 21
 US-09-863-971A-8
 ; Sequence 8, Application US/09863971A
 ; Patent No. 6641798
 ; GENERAL INFORMATION:
 ; APPLICANT: Achillefu, Samuel I.
 ; APPLICANT: Rajagopalan, Raghavan
 ; APPLICANT: Dorschow, Richard B.
 ; APPLICANT: Bugaj, Joseph E.
 ; APPLICANT: Mallinckrodt Inc.
 ; TITLE OF INVENTION: Tumor-Targeted Optical Contrast Agents
 ; FILE REFERENCE: MRD-65
 ; CURRENT APPLICATION NUMBER: US/09/863, 971A
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 09/484, 320
 ; PRIOR FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (1) .. (1)
 ; OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is completely synthesized.
 ; US-09-863-971A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 5; Conservative 0; Indels 0; Gaps 0; Matches 2; Other Information: Xaa at location 1 represents D-Lys. Artificial sequence is completely synthesized.
 ; US-09-863-971A-8

OY 2 PXRPyXL 8

Db 2 | ||| | PRRPYYL 8

RESULT 23
US-09-978-725A-8
Sequence 8, Application US/09978725A
PATENT INFORMATION:
PATENT No. 6761878
APPLICANT: Achilefu, Samuel I.
APPLICANT: Dorshow, Richard B.
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Bugaj, Joseph E.
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: Pathological Tissue Detection and Treatment Employing
FILE REFERENCE: MRD-73
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(8)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
OTHER INFORMATION: completely synthesized.
US-09-978-725A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 2 PRRPYYL 8

RESULT 24
US-09-528-200-177
Sequence 177, Application US/09528200
PATENT No. 6630570
GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: BECKER, ANDREAS
APPLICANT: WEDENMANN, BERTJAM
APPLICANT: HESSNITS, CARTSEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT FILING NUMBER: US/09/528 200
PRIORITY FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 194
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-528-200-194

Query Match 84.8%; Score 28; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 8.9;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 3 PRRPYYL 9

RESULT 25
US-09-2-28-200-194
Sequence 194, Application US/09528200
PATENT No. 6630570
GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: WEDENMANN, BERTJAM
APPLICANT: HESSNITS, CARTSEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT FILING NUMBER: DE 199 17 713.9
PRIORITY FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 194
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-2-28-200-177

Query Match 84.8%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 3 PRRPYYL 9

RESULT 26
US-08-141-314-6
Sequence 6, Application US/08141324
PATENT No. 5475097
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Phillip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
US-09-528-200-177

Query Match 84.8%; Score 28; DB 4; Length 9;

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/714,540
 FILING DATE: 1991-06-07
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Diane E.
 REGISTRATION NUMBER: 31,292
 REFERENCE/DOCKET NUMBER: 8500-0135.00
 TELEPHONE: 415-327-7250
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-714-540-8

Query Match
 Best Local Similarity 84.8%; Score 28; DB 1; Length 13;
 Matches 5; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;
 Db 7 PRRPYIL 13

RESULT 30
 US-08-428-488-11
 Sequence 117, Application US/08428488
 Patent No. 5624894

GENERAL INFORMATION:
 APPLICANT: BODOR, Nicholas S.
 TITLE OF INVENTION: BRAIN ENHANCED DELIVERY OF NEUROACTIVE
 NUMBER OF INVENTIONS: 1
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Pattern In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,137
 FILING DATE: 12-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,546
 FILING DATE: 14-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,831
 FILING DATE: 01-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/959,560
 FILING DATE: 13-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/641,720
 FILING DATE: 15-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 016197-000840US
 TELEPHONE: 415-576-0200
 INFORMATION FOR SEQ ID NO: 117:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 FEATURE: NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "p-Glu"
 US-08-747-137-117

Query Match 84.8%; Score 28; DB 2; Length 13;

Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRXPXL 8
Db 7 PRRPYTL 13

RESULT 32
US-08-737-299A-1
; Sequence 1, Application US/08737299A
; Patent No. 5952464
GENERAL INFORMATION:
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,299
FILING DATE: 21-JUL-1997
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02131
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jeffrey S. Boone
REGISTRATION NUMBER: 29284
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1 (314) 654-8955
TELEFAX: 1 (314) 654-3156
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLogy: not relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "PYROGLUTAMIC ACID"
US-08-737-299A-1
Query Match 84.8%; Score 28; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRXPXL 8
Db 7 PRRPYTL 13

RESULT 33
US-09-334-254A-1
; Sequence 1, Application US/09334254A
; Patent No. 619436
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7

Correspondence Address:
Addressee: Jeffrey S. Boone
Street: 675 McDonnell Blvd.
City: St. Louis
State: MO
Country: US
Zip: 63134
Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: PatentIn Release #1.0, Version #1.30
Current Application Data:
Application Number: US/09/334, 254A
Filing Date: 09/13/2000
Classification:
Prior Application Data:
Application Number: 08/737, 299
Filing Date: 21-JUL-1997
Attorney/Agent Information:
Name: Jeffrey S. Boone
Registration Number: 29284
Reference/Docket Number: M0863-WO-US
Telecommunication Information:
Telephone: 1 (314) 654-8955
Telefax: 1 (314) 654-3156
Information for Seq ID No: 1:
Sequence Characteristics:
Length: 13 amino acids
Type: amino acid
Strandedness: not relevant
Topology: not relevant
Molecule Type: peptide
Fragment Type: internal
Feature:
Name/Key: Modified-site
Location: 1
Other Information: /product= "PYROGLUTAMIC ACID"
US-09-334-254A-1
Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRXPXL 8
Db 7 PRRPYTL 13

RESULT 34
US-09-289-693-1
; Sequence 1, Application US/09289693
; Patent No. 6214790
GENERAL INFORMATION:
APPLICANT: Richelson, Elliott
APPLICANT: Cusack, Bernadette Marie
APPLICANT: Pang, Yuan-Ping
APPLICANT: McCormick, Daniel J.
APPLICANT: Faqu, Abdil
APPLICANT: Tyler, Beth Marie
APPLICANT: Boules, Mona
Title of Invention: NEO-TRYPTOPHAN
File Reference: 07039/141001
Current Application Number: US/09/289, 693
Current Filing Date: 1999-04-09
Earlier Application Number: US 60/112, 137
Earlier Filing Date: 1998-12-14
Earlier Application Number: US 60/098, 119
Earlier Filing Date: 1998-08-27
Earlier Application Number: US 60/092, 195
Earlier Filing Date: 1998-07-09
Earlier Application Number: US 60/081, 256
Earlier Filing Date: 1998-04-10

NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Syntheticly generated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = pyrrolidone carboxylic acid
; US-09-289-693-1
Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 7 PRRPYIL 13

RESULT 35
US-09-355-863-2
; Sequence 2, Application US/09355869
; Patent No. 631261
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF MALIGNANT
; TITLE OF INVENTION: HUMAN TUMOURS
; FILE REFERENCE: 1668-304
; CURRENT APPLICATION NUMBER: US/09/355,869
; CURRENT FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/01964
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: EP 97200297.6
; PRIOR FILING DATE: 1997-02-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This site is pyroglutamate.
; US-09-355-869-2
Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 7 PRRPYIL 13

RESULT 36
US-09-605-990-8
; Sequence 8, Application US/09605990
; Patent No. 634451
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Junita
; APPLICANT: Cruz, Jourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Salk Institute
; TITLE OF INVENTION: Conulakin-G, Analogs Thereof and Uses Therefor
; CURRENT APPLICATION NUMBER: US/09/420,797B
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130,661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128,561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105,015
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.

RESULT 37
US-09-420-797B-8
; Sequence 8, Application US/09420797B
; Patent No. 6366193
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Junita
; APPLICANT: Cruz, Jourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Salk Institute
; TITLE OF INVENTION: Conulakin-G, Analogs Thereof and Uses Therefor
; CURRENT APPLICATION NUMBER: US/09/420,797B
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130,661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128,561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105,015
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.

FEATURE: PEPTIDE
 NAME/KEY: PEPTIDE
 LOCATION: (1)
 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
 US-09-420-797B-8

Query Match Best Local Similarity 84.8%; Score 28; DB 3; Length 13;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXPYXL 8
 Db 7 PRPYYL 13

RESULT 38
 US-09-605-991-8
 Sequence 8 Application US/09605991
 Patent No. 648298
 GENERAL INFORMATION:
 APPLICANT: Craig, A. Grey
 APPLICANT: Griffen, David
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Watkins, Maren
 APPLICANT: Hillyard, David R.
 APPLICANT: Imperial, Julita
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Wagstaff, John D.
 APPLICANT: Layer, Richard T.
 APPLICANT: Jones, Robert M.
 APPLICANT: McCabe, R. Tyler
 APPLICANT: Cognetix, Inc.
 APPLICANT: University of Utah Research Foundation
 TITLE OF INVENTION: Contulakin-G, Analogs Thereof and Uses Therefor
 FILE REFERENCE: Contulakin-G CIP
 CURRENT APPLICATION NUMBER: US/09/609, 534
 CURRENT FILING DATE: 2000-06-30
 EARLIER APPLICATION NUMBER: US 60/130, 661
 EARLIER FILING DATE: 1999-04-23
 EARLIER APPLICATION NUMBER: US 60/128, 561
 EARLIER FILING DATE: 1999-04-09
 EARLIER APPLICATION NUMBER: US 60/105, 015
 EARLIER FILING DATE: 1998-10-20
 EARLIER APPLICATION NUMBER: US 09/420, 797
 EARLIER FILING DATE: 1999-10-19
 EARLIER APPLICATION NUMBER: US 09/ 09/
 EARLIER FILING DATE: 2000-06-29
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 8
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Bos sp.
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)
 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.

US-09-609-534-8
 Query Match Best Local Similarity 84.8%; Score 28; DB 4; Length 13;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXPYXL 8
 Db 7 PRPYYL 13

RESULT 40
 US-09-528-200-10
 Sequence 10 Application US/09528200
 Patent No. 6630570
 GENERAL INFORMATION:
 APPLICANT: LICHA, KAI
 APPLICANT: BECKER, ANDREAS
 APPLICANT: SEMMLER, WOLFHARD
 APPLICANT: WEIDENMANN, BERTRAM
 APPLICANT: HESSNLIUS, CARTSEN
 APPLICANT: VOLKMER-ENGERT, RUDOLF
 APPLICANT: SCHNEIDER-MERGEVER, JENS
 APPLICANT: BHARGAVA, SARAH
 TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
 FILE REFERENCE: SCH-1731
 CURRENT APPLICATION NUMBER: US/09/528, 200
 CURRENT FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: DE 199 17 713 9
 PRIOR FILING DATE: 1999-09-04
 NUMBER OF SEQ ID NOS: 196
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 10
 LENGTH: 13
 TYPE: PRT

RESULT 39
 US-09-609-534-8
 Sequence 8 Application US/09609534
 Patent No. 652021
 GENERAL INFORMATION:
 APPLICANT: Craig, A. Grey

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1) OTHER INFORMATION: pglu
; US-09-528-200-10

Query Match 84.8%; Score 28; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
| ||||
Db 7 PRRPyYL 13

Search completed: March 28, 2005, 08:39:01
Job time : 46 secs

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Om protein - protein search, using sw model

Run on:

March 28, 2005, 08:33:43 ; Search time 68 Seconds
(without alignments)
45.501 Million cell updates/sec

Title: US-10-036-918B-4
Perfect score: 33
Sequence: 1 XPKXRPYXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 2105692
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:
1: geneseqP1980B:*

2: geneseqP1990B:*

3: geneseqP2000B:*

4: geneseqP2010B:*

5: geneseqP2002B:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004B:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	90.9	104 3	AAG28479 Zea mays
2	29	87.9	8 4	AAB15440 Amino acid, Alanine
3	29	87.9	30 7	ADD15507 Predicted protein, Human
4	29	87.9	53 4	AAM88000 Human Immunoglobulin heavy chain
5	29	87.9	70 4	AASU7965 Propionibacter propionicum
6	29	87.9	70 6	ABM64484 Propionibacter propionicum
7	29	87.9	74 4	AASU5129 Propionibacter propionicum
8	29	87.9	74 6	ABM01648 Propionibacter propionicum
9	29	87.9	157 6	ADP5463 Human protein
10	29	87.9	157 6	ABP11840 Human glycoprotein
11	29	87.9	216 8	ADG319768 G-protein
12	29	87.9	281 6	ABU144652 Protein e
13	29	87.9	312 6	ABU6400 Protein e
14	29	87.9	314 6	ABP79282 N. gonorrhoeae
15	29	87.9	315 4	AAU35421 Human hemophillin
16	29	87.9	315 6	ABU59640 Protein e
17	29	87.9	315 6	ABU30234 Protein e
18	29	87.9	315 6	AAE30458 Hemophilus ducreyi
19	29	87.9	316 4	AAU36341 Pseudomonas aeruginosa
20	29	87.9	316 6	ABU38589 Protein e
21	29	87.9	317 6	AAU39034 Protein e
22	29	87.9	317 6	ABU2211 Protein e
23	29	87.9	319 4	AAU44555 B. coli C
24	29	87.9	319 4	AAU38304 Salmonella enterica
25	29	87.9	319 6	ABU27909 Protein e

26	29	29	87.9	319	6	ABU349488
27	29	29	87.9	319	6	ABU31682
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29	29	87.9	319	6	ABU37970	
30	30	29	87.9	319	6	ABU23166
31	29	29	87.9	319	6	ABU2657
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41	29	29	87.9	345	4	ADP00359
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213	28	28	87.9	3783	4	ADU16173
214	28	28	87.9	3783	4	ADU65764
215	28	28	87.9	3783	7	ADP06340
216	28	28	87.9	3783	7	ADP15500
217	28	28	87.9	3783	6	ADP040545
218	28	28	87.9	3783	6	ADP04210
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220	28	28	87.9	3783	7	ADP04580
221	28	28	87.9	3783	7	ADP00359
222	28	28	87.9	3783		

RESULT 1	
AAG28479	
ID	AAG28479 standard; protein; 104 AA.
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AC	AAG28479;
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DT	17-OCT-2000 (first entry)
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DE	Zea mays protein fragment SEQ ID NO: 33711.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression; control; promoter; termination sequence; corn.
KW	
OS	Zea mays subsp. mays.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PP	25-FEB-2000; 20000BP-00301439.
XX	
PR	25-FEB-1999; 99US-01211825P.
PR	05-MAR-1999; 99US-01231180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	05-MAY-1999; 99US-0130510P.
PR	23-APR-1999; 99US-0130891P.
PR	28-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-0132048P.
PR	11-MAY-1999; 99US-0132407P.
PR	14-MAY-1999; 99US-0132484P.
PR	14-MAY-1999; 99US-0132485P.
PR	06-MAY-1999; 99US-0132486P.
PR	06-MAY-1999; 99US-0132487P.
PR	07-MAY-1999; 99US-0132863P.
PR	19-MAY-1999; 99US-0134256P.
PR	14-MAY-1999; 99US-0134218P.
PR	14-MAY-1999; 99US-0134219P.
PR	14-MAY-1999; 99US-0134221P.
PR	14-MAY-1999; 99US-0134370P.
PR	18-MAY-1999; 99US-0134768P.
PR	19-MAY-1999; 99US-0134941P.
PR	20-MAY-1999; 99US-0135124P.
PR	21-MAY-1999; 99US-0135353P.
PR	24-MAY-1999; 99US-0135629P.
PR	25-MAY-1999; 99US-0136021P.
PR	27-MAY-1999; 99US-0136392P.
PR	28-MAY-1999; 99US-0136782P.
PR	01-JUN-1999; 99US-0137222P.
PR	03-JUN-1999; 99US-0137528P.
PR	04-JUN-1999; 99US-0137502P.
PR	07-JUN-1999; 99US-0137724P.
PR	10-JUN-1999; 99US-0138094P.
PR	10-JUN-1999; 99US-0138540P.
PR	10-JUN-1999; 99US-0138847P.
PR	14-JUN-1999; 99US-0139119P.
PR	16-JUN-1999; 99US-0139452P.
ALIGNMENTS	

	PR	13-AUG-1999;	990US-0148565P.
	PR	13-AUG-1999;	990US-0148684P.
	PR	16-AUG-1999;	990US-0149368P.
	PR	17-AUG-1999;	990US-0149175P.
	PR	18-AUG-1999;	990US-0149426P.
	PR	20-AUG-1999;	990US-0149722P.
	PR	20-AUG-1999;	990US-0149723P.
	PR	20-AUG-1999;	990US-0149929P.
	PR	21-AUG-1999;	990US-0149902P.
	PR	23-AUG-1999;	990US-014999P.
	PR	23-AUG-1999;	990US-0150566P.
	PR	23-AUG-1999;	990US-0150884P.
	PR	27-AUG-1999;	990US-0151065P.
	PR	27-AUG-1999;	990US-0151066P.
	PR	30-AUG-1999;	990US-0151080P.
	PR	31-AUG-1999;	990US-0151303P.
	PR	01-SEP-1999;	990US-0151930P.
	PR	07-SEP-1999;	990US-0152363P.
	PR	10-SEP-1999;	990US-0153070P.
	PR	13-SEP-1999;	990US-0153758P.
	PR	15-SEP-1999;	990US-0154018P.
	PR	16-SEP-1999;	990US-0154039P.
	PR	20-SEP-1999;	990US-0154779P.
	PR	22-SEP-1999;	990US-0155139P.
	PR	23-SEP-1999;	990US-0155486P.
	PR	28-SEP-1999;	990US-0155659P.
	PR	29-SEP-1999;	990US-015658P.
	PR	04-OCT-1999;	990US-0157117P.
	PR	05-OCT-1999;	990US-0157753P.
	PR	06-OCT-1999;	990US-0157865P.
	PR	08-OCT-1999;	990US-0158232P.
	PR	12-OCT-1999;	990US-0158369P.
	PR	13-OCT-1999;	990US-0159293P.
	PR	13-OCT-1999;	990US-0159294P.
	PR	13-OCT-1999;	990US-0159295P.
	PR	14-OCT-1999;	990US-0159329P.
	PR	14-OCT-1999;	990US-0159330P.
	PR	14-OCT-1999;	990US-0159331P.
	PR	14-OCT-1999;	990US-0159637P.
	PR	14-OCT-1999;	990US-0159638P.
	PR	18-OCT-1999;	990US-0159584P.
	PR	21-OCT-1999;	990US-0160741P.
	PR	21-OCT-1999;	990US-0160767P.
	PR	21-OCT-1999;	990US-0160768P.
	PR	21-OCT-1999;	990US-0160770P.
	PR	21-OCT-1999;	990US-0160814P.
	PR	21-OCT-1999;	990US-0160815P.
	PR	22-OCT-1999;	990US-0160980P.
	PR	22-OCT-1999;	990US-01610981P.
	PR	25-OCT-1999;	990US-0161040P.
	PR	25-OCT-1999;	990US-0161405P.
	PR	25-OCT-1999;	990US-0161406P.
	PR	26-OCT-1999;	990US-0161359P.
	PR	26-OCT-1999;	990US-0161360P.
	PR	26-OCT-1999;	990US-0161361P.
	PR	28-OCT-1999;	990US-0161920P.
	PR	28-OCT-1999;	990US-0161992P.
	PR	28-OCT-1999;	990US-0161993P.
	PR	29-OCT-1999;	990US-0162142P.
	Query Match	90.9%; Score 30; DB 3; Length 104;	
	Best Local Similarity	71.4%; Pred. No. 1.3e-02;	
	Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	2	PXRPyXL 8	
Db	8	PARPySL 14	
	RESULT 2		
	AAB31540		
	ID AAB31540 standard; peptide; 8 AA.		
	XX		
	AAC AAB31540;		
	AC		
	XX		
	DT	20-APR-2001 (first entry)	
	XX		
	DE	Amino acid sequence of a peptide analogue of neurotensin.	
	XX		
	Neurotensin; neurotensin receptor; neurotensin analogue; tumour; KW small cell lung carcinoma; exocrine pancreatic cancer; Ewing sarcoma; KW meningioma; medulloblastoma; astrocytoma.		
	OS	Synthetic.	
	XX		
	FH		
	Key-difference	Location/Qualifiers	
	FT	"D-form residue"	
	FT	Modified-site 1 /note= "D- form residue"	
	FT	Modified-site 2 /note= "Diethylenetriamine pentaacetic acid (DTPA)"	
	FT	Modified-site 3 /note= "attached"	
	FT	Modified-site 4 /note= "(N-amidinopiperidinyl) homoalanine or (N-	
	FT	Modified-site 5 /note= "amidinopiperidinyl homoalanine"	
	FT	Modified-site 6 /note= "t-butylglycine"	
	FT	Modified-site 7 /note= "-OH attached"	
	FT	Modified-site 8 /note= "-OH attached"	
	XX		
	PN	WO200078796-A2.	
	XX		
	PD		
	XX		
	XX		
	22-JUN-2000;	20000W0-US017509.	
	XX		
	PR	24-JUN-1999; 990US-0140913P.	
	PR	21-JUN-2000; 20000US-0213068P.	
	XX		
	PA	(MILCW) MALLINCKRODT INC.	
	PA	(SRIN/) SRINTVASAN A.	
	PA	(ERIO/) ERION J L.	
	PA	(SCHM/) SCHMIDT M A.	
	XX		
	PI	Srinivasan A, Erion JL, Schmidt MA;	
	XX		
	DR	WPI; 2001-102696/11.	
	XX		
	PT	Novel neurotensin peptides for diagnosing and treating tumors such as PT small cell lung carcinomas, contain Arginine mimics.	
	PS	Claim 14; Page 33; 39pp; English.	
	XX		
	CC	The present sequence represents a peptide analogue of neurotensin.	
	CC	Neurotensin (see AAB31521) is a small peptide which is isolated from bovine hypothalamus. High concentrations of neurotensin receptors are found in several tumour cells. However, neurotensin has a short half-life. The neurotensin analogues of the invention contain arginine mimics, which results in increased serum stability and stability. The neurotensin analogues have selective affinity for neurotensin receptors. The peptide analogues are also resistant to enzymatic degradation. The IC50 value of the neurotensin analogue is comparable to native neurotensin. Neurotensin analogues are used for diagnosis and treatment of tumors, such as small cell lung carcinoma, exocrine pancreatic cancer, Ewing sarcoma, meningioma, medulloblastoma or astrocytoma by administering the peptide	
	CC	Sequence 8 AA;	
	SO	Query Match 87.9%; Score 29; DB 4; Length 8;	
	Matches	Best Local Similarity 85.7%; Pred. No. 1.8e+06; Mismatches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	2	PXRPyXL 8	

RESULT 3		2 PARPYKL 8	
ADD15507		Best Local Similarity 71.4%; Pred. No. 58; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
XX	XX	QY	2 PXR PYKL B
AC	AC	Db	16 PQRPYKL 22
XX	XX	RESULT 4	
DR	DR	AAMB8000	
DE	DE	ID AAM88000	standard; protein; 53 AA.
Predicted epitopic region of the E_coli AccA protein (seqID 72).		XX	
KW	KW	AC	AAMB8000;
microbial; antimicrobial; membrane biosynthesis; pathogenic;		XX	
immunological response; vaccination; surface disinfectant;		XX	
KW	KW	DT	07-NOV-2001 (first entry)
personal hygiene application; food preservative; AccA; acetyl-CoA carboxylase carboxyl transferase subunit alpha; epitope.		XX	Human immune/haemopoietic antigen SEQ ID NO:15593.
XX	XX	XX	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
OS	OS	XX	cytostatic; gene therapy; vaccine; metastasis.
Escherichia coli.		OS	Homo sapiens.
XX	XX	XX	
PN	PN	PN	W0200305007-A2.
XX	XX	PN	
PD	PD	XX	09-AUG-2001.
XX	XX	PP	17-JAN-2001; 2001WO-US001354.
PR	PR	XX	
26-OCT-2001; 2001US-0339924P.		PR	31-JAN-2000; 2000US-0179065P.
PR	PR	PR	04-FEB-2000; 2000US-0180628P.
29-OCT-2001; 2001US-0350973P.		PR	24-FEB-2000; 2000US-0184664P.
PR	PR	PR	02-MAR-2000; 2000US-0186350P.
30-OCT-2001; 2001US-030924P.		PR	16-MAR-2000; 2000US-0189874P.
PR	PR	PR	17-MAR-2000; 2000US-0190076P.
21-SEP-2001; 2001US-0323992P.		PR	18-APR-2000; 2000US-0198123P.
PR	PR	PR	19-MAY-2000; 2000US-0205515P.
21-SEP-2001; 2001US-0324152P.		PR	07-JUN-2000; 2000US-0209467P.
PR	PR	PR	28-JUN-2000; 2000US-0214886P.
25-SEP-2001; 2001US-0334692P.		PR	07-JUL-2000; 2000US-0216647P.
PR	PR	PR	07-JUL-2000; 2000US-0216880P.
26-OCT-2001; 2001US-0339924P.		PR	11-JUL-2000; 2000US-0217487P.
PR	PR	PR	14-JUL-2000; 2000US-0217490P.
27-NOV-2001; 2001US-0333666P.		PR	26-JUL-2000; 2000US-0220963P.
PR	PR	PR	26-JUL-2000; 2000US-0220964.
18-DEC-2001; 2001US-0341776P.		PR	14-AUG-2000; 2000US-0224518P.
PR	PR	PR	14-AUG-2000; 2000US-022513.
19-DEC-2001; 2001US-0341949P.		PR	14-AUG-2000; 2000US-0225214P.
PR	PR	PR	14-AUG-2000; 2000US-0225266P.
XX	XX	PR	14-AUG-2000; 2000US-0225267.
PA	PA	PR	14-AUG-2000; 2000US-0225268P.
(AFFI-) AFFINITY PHARM INC.		PR	14-AUG-2000; 2000US-0225270P.
XX	XX	PR	14-AUG-2000; 2000US-0225447.
PR	PR	PR	14-AUG-2000; 2000US-0225757P.
XX	XX	PR	14-AUG-2000; 2000US-0225759P.
PR	PR	PR	18-AUG-2000; 2000US-0226279P.
XX	XX	PR	22-AUG-2000; 2000US-0226681P.
CC	CC	PR	22-AUG-2000; 2000US-0226686P.
CC	CC	PR	22-AUG-2000; 2000US-0227182P.
CC	CC	PR	23-AUG-2000; 2000US-0227009P.
CC	CC	PR	30-AUG-2000; 2000US-022824P.
CC	CC	PR	01-SEP-2000; 2000US-0228287P.
CC	CC	PR	01-SEP-2000; 2000US-0229343P.
CC	CC	PR	01-SEP-2000; 2000US-0229344P.
CC	CC	PR	01-SEP-2000; 2000US-0223345P.
CC	CC	PR	05-SEP-2000; 2000US-0228509P.
SQ	Sequence 30 AA;	PR	05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 05-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0233163P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-02331413P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233163P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 02-OCT-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-02446474P.
 PR 08-NOV-2000; 2000US-02446475P.
 PR 08-NOV-2000; 2000US-02446476P.
 PR 08-NOV-2000; 2000US-02446477P.
 PR 08-NOV-2000; 2000US-0244652P.
 PR 08-NOV-2000; 2000US-02446525P.
 PR 08-NOV-2000; 2000US-02446526P.
 PR 08-NOV-2000; 2000US-02446527P.
 PR 08-NOV-2000; 2000US-02446528P.
 PR 08-NOV-2000; 2000US-02446532P.
 PR 08-NOV-2000; 2000US-0244660P.
 PR 08-NOV-2000; 2000US-02446610P.
 PR 08-NOV-2000; 2000US-02446611P.
 PR 08-NOV-2000; 2000US-02446613P.
 PR 17-NOV-2000; 2000US-02449207P.
 PR 17-NOV-2000; 2000US-02449213P.
 PR 17-NOV-2000; 2000US-02449214P.
 PR 17-NOV-2000; 2000US-02449215P.
 PR 17-NOV-2000; 2000US-02449216P.
 PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 05-DEC-2000; 2000US-0249299P.
 PR 05-DEC-2000; 2000US-0251479P.
 PR 05-DEC-2000; 2000US-0251850P.
 PR 05-DEC-2000; 2000US-025160P.
 PR 05-DEC-2000; 2000US-0251860P.
 PR 08-DEC-2000; 2000US-0251980P.
 PR 11-DEC-2000; 2000US-0254090P.
 PR 05-JAN-2001; 2001US-0259670P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PT Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-49342652.
 DR N-PSDB; AAK60781.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX Claim 11; SEQ ID NO 15593; 3071pp + Sequence Listing; English.
 XX AAK54951 to AAK6702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytotoxic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases. AAK6703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM02169 represent sequences used in the exemplification of the present invention
 XX Sequence 53 AA;
 Query Match 87.9%; Score 29; DB 4; Length 53;
 Best Local Similarity 85.7%; Pred. No. 1e02; Matches 6; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXRDXL 8
 DB 44 PXRDXL 50

RESULT 5
 AAU67965
 ID AAU67965 standard; protein; 70 AA.
 XX AAU67965;
 AC
 DT 27-FEB-2002 (first entry)
 XX Propionibacterium acnes immunogenic protein #28861.
 XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertrichosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

XX WO200181581-A2.

PN PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.

XX PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PT L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI; 2001-616774/71.

PT N-PSDB; AAS55773.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX PS Example 1; SEQ ID NO 29160; 1069pp; English.

CC Sequences AAU39105-AU8017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertrichosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies.
 CC specific for P. acnes protein. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 70 AA;

Query Match 87.9%; Score 29; DB 4; Length 70;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; MisMatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 38 PYRPySL 44

RESULT 6
 ABM64484 ABM64484 standard; protein; 70 AA.

AC XX
 DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #29160.

XX PN Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PR 24-APR-2003.

XX PD 11-OCT-2002; 2002WO-US032777.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Vailleve-Douglas J;

XX DR WPI; 2003-381789/36.

XX N-PSDB; ACF64702.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.

XX PS Example 1; SEQ ID NO 29160; 1481pp; English.

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM3524-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 via this method; a vaccine composition comprising P. acnes polypeptides,
 CC polynucleotides; antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide; a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 70 AA;

Query Match 87.9%; Score 29; DB 6; Length 70;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; MisMatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 38 PYRPySL 44

RESULT 7
 AAU65129
 ID AAU65129 standard; protein; 74 AA.

AC XX

DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #26025.
 XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #26324.
 XX Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 OS Propionibacterium acnes.
 XX PN WO2001B1581-A2.
 XX PD 01-NOV-2001.
 XX PR 20-APR-2001; 2001WO-US012865.
 XX PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 XX PR 07-JUL-2000; 2000US-0216747P.
 PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI Li maisonneuve J, Zhang Y, Jen S, Carter D;
 DR XX WPI; 2001-616774/71.
 DR N-PSDB; AAS29660.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 26324; 1069pp; English.
 PS Sequences AAU39105-AAU8017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperosis and ostemyelitis), uveitis and endophthalmitis;
 CC P. acnes is also involved in infections of bone, joints and the central
 nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 74 AA;

Query Match 87.9%; Score 29; DB 4; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 QY 2 PXRPyXL 8
 ID ABM61648
 DB 38 PYRPySL 44

Query Match 87.9%; Score 29; DB 6; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
 QY 2 PXRPyXL 8
 ID ABM61648
 DB 38 PYRPySL 44

Query Match 87.9%; Score 29; DB 6; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
 QY 2 PXRPyXL 8
 ID ABM61648
 DB 38 PYRPySL 44

DT 20-OCT-2003 (first entry)
 XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #26324.
 XX Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW immunosimulant; immune response; vaccine.
 OS Propionibacterium acnes.
 XX PN WO2003033515-A1.
 XX PD 24-APR-2003.
 XX PR 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieve-Douglas J;
 XX DR WPI; 2003-381789/36.
 XX DR N-ISDB; ACP64589.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Example 1; SEQ ID NO 26324; 1481pp; English.
 CC The invention relates to an isolated polynucleotide (ACFP4435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (AM35624-AB64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 74 AA;

ID ADA54863 standard; protein; 157 AA.
 XX
 AC ADA54863;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DB Human protein, SEQ ID 2431.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PT (TIFYU-) UNIV FUDAN.
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (REBLI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53224.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 2431; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA542433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
 CC Sequence 157 AA;
 XX
 Query Match 87.9%; Score 29; DB 6; Length 157;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 Db 43 PNRPyTL 49
 XX
 RESULT 11
 ADG19768
 ID ADG19768 standard; protein; 216 AA.
 XX
 AC ADG19768;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 G-Protein coupled receptor domain related consensus seq id 106.
 DE cyrostatic; nephrotropic; antiinflammatory; cardiant; respiratory;
 KW gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
 KW 18636; 2466; 43238; 1983; 52881; 2391; 43449; 50289; 52872; 26908;
 KW cellular proliferative disorder; brain disorder; renal disorder;
 KW kidney disorder; inflammatory disorder; cardiovascular disorder;
 KW liver disorder; intestinal disorder; respiratory disorder;
 KW angiogenic disorder; human; G protein coupled receptor; GPCR;
 KW protein domain.
 XX
 OS Unidentified.
 XX
 US2003215860-A1.
 PN
 PD 20-NOV-2003.
 XX
 PF 03-APR-2003; 2003US-00407079.
 XX
 PR 29-FEB-2000; 2000US-0186059P.
 PR 24-MAR-2000; 2000US-0191845P.
 PR 22-MAY-2000; 2000US-0206019P.
 PR 17-NOV-2000; 2000US-00715700.
 PR 20-FEB-2001; 2001US-00796338.
 PR 22-MAY-2001; 2001US-00863200.
 PR 22-AUG-2001; 2001US-0314041P.
 PR 22-AUG-2001; 2001US-0314185P.
 PR 21-AUG-2002; 2002US-00225094.
 PR 22-AUG-2002; 2002US-00226102.

PR 15-OCT-2002; 2002US-00372417.
 PR 29-OCT-2002; 2002US-00282837.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;
 XX
 DR WPI; 2004-010777/01.

XX
 PT New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or 26908, useful in preparing a composition for treating e.g., cellular proliferative, brain, kidney, inflammatory or angiogenic disorder.

XX
 PS Disclosure; SEQ ID NO 106; 163PP; English.

XX
 CC The invention describes a new isolated 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a sequence comprising 939-3489 bp or its fragment comprising at least 15 nucleotides; a sequence encoding a polypeptide comprising a sequence having 223-832 amino acids, or its allelic variant or fragment comprising at least 15 contiguous amino acids; or a sequence that hybridizes with (1) under stringent conditions. The nucleic acid or polypeptide is useful in preparing a composition for treating a disorder characterized by aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or 26908 activity e.g., cellular proliferative, brain, kidney, inflammatory, cardiovascular, liver, intestinal, respiratory or angiogenic disorder. This is the amino acid sequence of a human G-protein coupled receptor 32 (GPR32), polypeptide used in the characterisation of novel human G-protein coupled receptor 26908.

XX
 SQ Sequence 216 AA;

Query Match 87.9%; Score 29; DB 8; Length 216;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 AC
 XX
 QY 2 PXRRYXL 8
 DB 191 PDRPYSL 197

RESULT 12
 ABU44862
 ID ABU44862 standard; protein; 281 AA.
 XX
 AC ABU44862;
 XX
 DT 15-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #30389.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Salmonella paratyphi*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 03-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PR (ELIT-) ELITRA PHARM INC.
 XX
 KW Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu RH;
 XX
 PR

DR WPI; 2003-029926/02.
 DR N-PSDB; ACA4873Z.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 25; SEQ ID NO 72786; 176PP; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 281 AA;

Query Match 87.9%; Score 29; DB 6; Length 281;
 Best Local Similarity 71.4%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 AC
 XX
 QY 2 PXRRYXL 8
 DB 33 PORPYTL 39

RESULT 13
 ABU26400
 ID ABU26400 standard; protein; 312 AA.
 XX
 AC ABU26400;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #11927.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS *Campylobacter jejuni*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.

PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 05-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PT Yamamoto R, Forsyth RA, Xu HH;
 XX Wall D, Trawick JD, Carr GJ;
 DR WPI; 2003-029926/02.
 DR N-PSDB; AC2A0270.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 54324; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the antisense
 CC encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway; (8)
 required for proliferation, or that inhibits cellular proliferation or the biological
 CC pathway in which the test compound that inhibits proliferation of an
 CC or a gene on which the test compound that inhibits proliferation lies
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC parent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC http://wipo.int/pub/published_pct_sequences

XX Sequence 312 AA;

Query Match 87.9%; Score 29; DB 6; Length 314;
 Best Local Similarity 71.4%; Pred. No. 6.7e+02; Mismatches 0; Indels 0; Gap 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gap 0;

QY 2 PXRPyXL 8
 Db 62 PQRPyTL 68

RESULT 15
 AAU35421
 ID AAU35421 standard; protein; 315 AA.
 AC AAU35421;
 XX DT 14-FEB-2002 (first entry)
 XX DE Haemophilus influenzae cellular proliferation protein #62.
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 XX
 OS *Haemophilus influenzae*.
 XX
 PN WO2001170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191073P.
 PR 23-MAY-2000; 2000US-020684P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-0242573P.
 PR 27-NOV-2000; 2000US-025362P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269303P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX
 OS *Neisseria gonorrhoeae*.
 XX
 PN WO200279243-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 12-FEB-2002; 2002WO-1B002069.
 XX
 PR 12-FEB-2001; 2001GB-00003424.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a
 PT medicament for treating or preventing *N. gonorrhoeae* infection.
 XX
 PS Disclosure; Page 561; 815pp; English.

The present invention relates to proteins from *Neisseria gonorrhoeae*.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 manufacture of a medicament for treating or preventing *N. gonorrhoeae*
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736; ABP81046 represent nucleic acid
 CC molecules of the invention
 XX Sequence 314 AA;

Query Match 87.9%; Score 29; DB 6; Length 314;
 Best Local Similarity 71.4%; Pred. No. 6.7e+02; Mismatches 0; Indels 0; Gap 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gap 0;

QY 2 PXRPyXL 8
 Db 62 PQRPyTL 68

RESULT 15
 AAU35421
 ID AAU35421 standard; protein; 315 AA.
 AC AAU35421;
 XX DT 14-FEB-2002 (first entry)
 XX DE Haemophilus influenzae cellular proliferation protein #62.
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 XX
 OS *Haemophilus influenzae*.
 XX
 PN WO2001170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191073P.
 PR 23-MAY-2000; 2000US-020684P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-0242573P.
 PR 27-NOV-2000; 2000US-025362P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269303P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

RESULT 14
 ABP79282
 ID ABR79282 standard; protein; 314 AA.
 XX
 AC ABR79282;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE *N. gonorrhoeae* amino acid sequence SEQ ID 5094.
 XX
 KW Antibacterial; infection; vaccine; gene therapy.

XX	Haselbeck R,	Ohsen KL,	Zyskind JW,	Wall D,	Trawick JD,	Carr GJ;	DR
PT	Yamamoto RT;	Xu HH;					WPI; 2003-029926/02.
XX							N-PSDB; AAC43510.
DR							New antisense nucleic acids, useful for identifying proteins or screening
PT							for homologous nucleic acids required for cellular proliferation to
PT							isolate candidate molecules for rational drug discovery programs.
XX							XX
PR							Claim 25; SEQ ID NO 67564; 176bp; English.
PT							New polymucleotides for the identification and development of
XX							PT antibiotics, comprise sequences of antisense nucleic acids.
PS							Example 3; SEQ ID NO 11014; 511bp; English.
XX							The invention relates to antisense inhibitors of genes essential to
CC							prokaryotic cellular proliferation, their use in identifying the genes,
CC							their use in the discovery of novel antibiotics, the essential genes
CC							encoding a polypeptide whose expression is inhibited by the antisense
CC							nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC							polypeptide or its fragment whose expression is inhibited by the
CC							antisense nucleic acid; (4) an antibody capable of specifically binding
CC							the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC							proliferation or the activity of a gene in an operon required for
CC							proliferation; (7) identifying a compound that influences the activity of
CC							the gene product or that has an activity against a biological pathway
CC							required for proliferation, or that inhibits cellular proliferation; (8)
CC							identifying a gene required for cellular proliferation or the biological
CC							pathway in which a proliferation-required gene or its gene product lies
CC							or a gene on which the test compound that inhibits proliferation of an
CC							organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC							compound's activity; (11) a culture comprising strains in which the gene
CC							product is overexpressed or underexpressed; (12) determining the extent
CC							to which each of the strains is present in a culture or collection of
CC							strains; or (13) identifying the target of a compound that inhibits the
CC							proliferation of an organism. The antisense nucleic acids are useful for
CC							identifying protein or screening for homologous nucleic acids required
CC							for cellular proliferation to isolate candidate molecules for rational
CC							drug discovery programs, or for screening homologous nucleic acids
CC							required for proliferation in cells other than S. aureus, S. typhimurium,
CC							K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC							the target prokaryotic essential genes. Note: The sequence data for this
CC							patent did not form part of the printed specification, but was obtained in
CC							electronic format directly from WPO at
CC							ftp.wipo.int/pub/published_pct_sequences
XX							SQ
XX							Sequence 315 AA;
RESULT 16							
Query Match	87.9%	Score 29;	DB 4;	Length 315;			
ID	ABU39640	standard; protein; 315 AA.					
XX							
AC	ABU39640;						
XX							
DT	19-JUN-2003	(first entry)					
DE	Protein encoded by Prokaryotic essential gene; cell proliferation; drug design.						
KW	Pseudomonas putida.						
XX							
XX	WO20027183-A2.						
PD	03-OCT-2002.						
XX							
PF	21-MAR-2002; 2002WO-US009107.						
XX							
PR	21-MAR-2001; 2001US-00815242.						
PR	06-SEP-2001; 2001US-00948993.						
PR	25-OCT-2001; 2001US-0342923P.						
PR	08-FEB-2002; 2002US-000712851.						
PR	06-MAR-2002; 2002US-0362699P.						
XX							
PA	(ELIT-) ELITRA PHARM INC.						
XX							
PT	Wang L, Zamudio C, Malone C, Haselbeck R, Ohsen KL, Zyskind JW;						
PT	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forbyth RA, Xu HH;						
XX							
PR	21-MAR-2001; 2001US-00815242.						
PR	21-MAR-2002; 2002WO-US009107.						
PR	21-MAR-2001; 2001US-00815242.						

PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forbyth RA, Xu HH;
 XX
 DR WPI; 2003-029296/02.
 DR N-PSDB; ACA3104.
 XX
 PS Claim 25; SEQ ID NO 58158; 176pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation or the biological
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX Sequence 315 AA;

Query Match Best Local Similarity Score 29; DB 6; Length 315;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 66 PNRPYPTL 72

SQ Sequence 315 AA;

Query Match Best Local Similarity Score 29; DB 6; Length 315;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 19
 ID AAU36341
 ID AAU36341 standard; protein; 316 AA.
 AC
 XX
 AAU36341;
 DT 14-FEB-2002 (first entry)
 XX
 DE Pseudomonas aeruginosa cellular proliferation protein #331.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Pseudomonas aeruginosa.
 XX
 WO200170955-A2.
 XX
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-019107P.
 PR 23-MAY-2000; 2000US-020684P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-024257P.
 PR 27-NOV-2000; 2000US-025362P.
 PR 22-DEC-2000; 2000US-025793P.

RESULT 18
 AAE30458
 ID AAE30458 standard; protein; 315 AA.
 AC
 XX
 AAE30458;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DB **Haemophilus influenzae acetyl coa carboxylase protein.**
 XX
 KW Virulence; veterinary; infection; pneumonia; antimicrobial drug; vaccine;

PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zykind JW;
 XX DR WPI; 2001-611495/70.
 PR N-PSDB; AAC54200.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 11934; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
 CC *coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 316 AA;

Query Match 87.9%; Score 29; DB 4; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 20
 ABU38589
 ID ABU38589 standard; protein: 316 AA.
 XX
 AC ABU38589;
 XX DT 19-JUN-2003 (first entry)
 DB Protein encoded by Prokaryotic essential gene #24116.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Pseudomonas aeruginosa*.
 XX WO200277183-A2.
 XX PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US09107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0342699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

PR Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-028296/02.
 PR N-PSDB; ACA42459.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 66513; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) providing a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 316 AA;

Query Match 87.9%; Score 29; DB 6; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 21
 ABU39034
 ID ABU39034 standard; protein: 317 AA.
 XX
 AC ABU39034;
 XX DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #24561.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Pasteurella multocida*.
 XX PN WO0277183-A2.
 XX PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 05-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 05-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA42904.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 PT
 XX
 PS Claim 25; SEQ ID NO 66958; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 317 AA;

SQ Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPYXL 8
 DB 68 PNRPYTL 74

RESULT 22

Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPYXL 8
 DB 69 PRRPYTL 75

DR Protein encoded by Prokaryotic essential gene #27738.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Pseudomonas Syringae.
 OS
 PN WO20027183-A2.
 PR 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX PD
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA46081.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 70135; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 317 AA;

SQ Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPYXL 8
 DB 69 PRRPYTL 75

RESULT 23
 AAU34455
 ID AAU34455 standard; protein; 319 AA.
 AC AAU34455;
 XX
 DT 14-FEB-2002 (first entry)
 DE E. coli cellular proliferation protein #36.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Escherichia coli.
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 XX
 DR WPI; 2001-611495/70.
 XX
 PT New polynucleotides for the identification and development of
 antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 10048; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 319 AA;

Query Match 87.9%; Score 29; DB 4; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPYXL 8
 Db 70 PQRPTL 76

RESULT 24
 AAU38304
 ID AAU38304 standard; protein; 319 AA.
 AC AAU38304;
 XX
 DT 14-FEB-2002 (first entry)
 DE *Salmonella typhi* cellular proliferation protein #195.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS *Salmonella typhi*.
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 XX
 DR WPI; 2001-611495/70.
 XX
 PT New Polynucleotides for the identification and development of
 antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 13897; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 319 AA;

Query Match 87.9%; Score 29; DB 4; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPYXL 8
 Db 70 PQRPTL 76

RESULT 25
 ABU27909
 ID ABU27909 standard; protein; 319 AA.
 XX
 AC ABU27909;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #13436.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Enterobacter cloacae.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00948993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA31779.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 PT Claim 25; SEQ ID NO 55833; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

RESULT 26
 ABU48247
 ID ABU48247 standard; protein; 319 AA.
 XX AC ABU48247;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #33774.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS *Salmonella typhi*.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00948993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA32117.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 76171; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

CC for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

CC Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2;

QY 2 PXRPyXL 8
Db 70 PQRPtL 76

RESULT 27

ABU37156
ID ABU37156 Standard; protein; 319 AA.

AC ABU37156;
XX DT 23-OCT-2003 (revised)
XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #22683.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Neisseria gonorrhoeae.
OS Neisseria gonorrhoeae.

XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PR 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
DR N-P5DB; ACRA41026.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
PT Isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 65000; 1766PP; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS Field)

CC Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2;

QY 2 PXRPyXL 8
Db 67 PQRPtL 73

RESULT 28

ABU4948B
ID ABU4948B Standard; protein; 319 AA.

AC ABU4948B;
XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #35015.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Vibrio cholerae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PR 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
DR N-P5DB; ACRA53358.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 77412; 1766PP; English.

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best local Similarity 71.4%; Pred. No. 6.8e+02; OS ABU31682
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 29

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best local Similarity 71.4%; Pred. No. 6.8e+02; OS ABU31682
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 AC ABU31682;
 XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #17209.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Klebsiella pneumoniae.

XX WO200271183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00348993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELTRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 XX Yamamoto R, Forsyth RA, Xu HH;
 PI Wall D, Trawick JD, Carr GA;
 XX PR 21-MAR-2001; 2001US-00815242.

DR WPI; 2003-029926/02.
 CC N-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

DR WPI; 2003-029926/02.

XX XN-PSDB; ACA35552.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

PR 06-SEP-2001; 2001US-00948993.
 PR 23-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 N-ISDB; ACA4515.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 PT
 XX
 PS Claim 25; SEQ ID NO 68369; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 319 AA;

Query Match Best local Similarity 87.9%; Score 29; DB 6; Length 319; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 70 PLRPyTL 76

RESULT 31

ABU5047
 ID ABU50047 Standard; protein; 319 AA.
 AC ABU50047;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #35574.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
 OS *Versinia pestis*.
 XX WO200271183-A2.
 PN
 XX PD 03-OCT-2002.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 N-ISDB; ACA53917.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 PS Claim 25; SEQ ID NO 77971; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 319 AA;

Query Match Best local Similarity 87.9%; Score 29; DB 6; Length 319; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 70 PLRPyTL 76

RESULT 32

ABU37970
ID ABU37970 standard; protein; 319 AA.
AC ABU37970;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #23497.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Neisseria meningitidis.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PA (ELIT-) ELITRA PHARM INC.
XX PT Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; WPI; 2003-0329926/02.
XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 65894; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation or an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences
SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; GapB 0;
AC ABU47369;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #32896.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PA (ELIT-) ELITRA PHARM INC.
XX PT Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; WPI; 2003-0329926/02.
XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 7293; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 319 AA;

RESULT 34
 ABU15268 ID ABU15268 standard; protein; 319 AA.
 XX AC ABU15268:
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #795.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Escherichia coli.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00848993.
 PR 22-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELT-) ELTTRA PHARM INC.

RESULT 35
 ADD15500 ID ADD15500 standard; protein; 319 AA.
 XX AC ADD15500:
 XX DT 15-JAN-2004 (first entry)
 XX DE Escherichia coli AccA protein (SeqID 65).
 KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
 KW immunological response; vaccination; surface disinfectant;
 KW personal hygiene application; food preservative; enzyme; AccA;
 KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 XX OS Escherichia coli.
 XX PN WO2003025007-A2.
 XX PD 27-MAR-2003.
 XX PF 20-SEP-2002; 2002WO-CA001428.
 XX PR 21-SEP-2001; 2001US-0323992P.
 PR 21-SEP-2001; 2001US-0324152P.
 PR 25-SEP-2001; 2001US-0324692P.
 PR 26-OCT-2001; 2001US-0339924P.
 PR 29-OCT-2001; 2001US-0350973P.
 PR 30-OCT-2001; 2001US-0340924P.
 PR 27-NOV-2001; 2001US-0333660P.
 PR 18-DEC-2001; 2001US-0341736P.
 PR 18-DEC-2001; 2001US-0341778P.
 PR 19-DEC-2001; 2001US-0341949P.
 XX PA (AFFI-) AFFINITY PHARM INC.

XX PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
 PI Donagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansouri K;
 PI McDonald M, Pinder B, Viola C, Wrezel O;
 DR WPI; 2003-468119-44.
 DR N-PSDB; ADD15499.
 XX PT Novel crystallized recombinant polypeptides from *Staphylococcus aureus*,

CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiting a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 319 AA;

RESULT 34
 ABU15268 ID ABU15268 standard; protein; 319 AA.
 XX AC ABU15268:
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #795.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Escherichia coli.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00848993.
 PR 22-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELT-) ELTTRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACC19138.
 XX PR New antisense nucleic acids, useful for identifying proteins or screening
 PR for homologous nucleic acids required for cellular proliferation to
 PR isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 43192; 176pp; English.
 XX CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation or the biological
 CC identifying a gene required for cellular proliferation or the biological

PT Streptococcus pneumoniae and Escherichia coli and which are involved in
 PT membrane biosynthesis, useful as targets for pathogenic bacteria.
 XX
 PS Claim 86; SEQ ID NO 65; 325pp; English.
 XX
 CC This invention relates to the structural and functional characterisation
 CC of microbial polypeptides from *Staphylococcus aureus* (*S. aureus*),
 CC *Streptococcus pneumoniae* (*S. pneumoniae*) and *Escherichia coli* (*E. coli*)
 CC that provide novel antimicrobial targets. Specifically, it refers to
 CC polypeptides that are involved in membrane biosynthesis, which play a
 CC critical role in the life cycle and viability of their pathogenic species
 CC of origin, and hence provide valuable drug targets. Furthermore, the
 CC invention describes modified version of these proteins that facilitate
 CC characterisation by labelling with isotopic or heavy atoms, and also
 CC fusion proteins. These proteins provide structural and functional
 CC information to aid the discovery of therapeutic molecules to treat
 CC disorders associated with a particular pathogenic species. As such, they
 CC are useful for inducing an immunological response in an individual and as
 CC an antigen for vaccination purposes. The polypeptides are also useful for
 CC developing antimicrobial agents for use as surface disinfectants,
 CC personal hygiene applications and as food preservatives or in treating
 CC food products to eliminate potential pathogens. This polypeptide sequence
 CC is the ACCA protein encoded by DNA predicted from the genomic sequence of
 CC *E. coli* acetyl-CoA carboxylase carboxyl transferase subunit alpha of the
 CC invention.
 XX SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 7; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 70 PORPyYL 76

RESULT 36
 ADD15502 DE Escherichia coli Acca protein (SeqID 67).
 XX
 XX DE Escherichia coli Acca protein (SeqID 67).
 XX KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
 KW immunological response; vaccination; surface disinfectant;
 KW personal hygiene application; food preservative; enzyme; Acca;
 KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 XX OS Escherichia coli.
 XX PN WO2003025007-A2.
 XX DT 15-JAN-2004 (first entry).
 XX
 XX DE Escherichia coli Acca protein (SeqID 67).
 XX KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
 KW immunological response; vaccination; surface disinfectant;
 KW personal hygiene application; food preservative; enzyme; Acca;
 KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 XX OS Escherichia coli.
 XX PN WO2003025007-A2.
 PR 21-SEP-2001; 2001US-0333992P.
 PR 21-SEP-2001; 2001US-0324152P.
 PR 25-SEP-2001; 2001US-0334692P.
 PR 26-OCT-2001; 2001US-0339924P.
 PR 29-OCT-2001; 2001US-0350973P.
 PR 30-OCT-2001; 2001US-0340924P.
 PR 27-NOV-2001; 2001US-0333666P.
 PR 18-DEC-2001; 2001US-0341732P.
 PR 18-DEC-2001; 2001US-0341776P.
 PR 19-DEC-2001; 2001US-0341949P.
 XX PA (AFPI-) AFFINUM PHARM INC.

RESULT 37
 ABU40545 DE ABU40545 standard; protein; 320 AA.
 XX AC ABU40545;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #26072.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Proteus sp.
 XX PN WO200277183-A2.
 XX DT 03-OCT-2002.
 XX DE 21-MAR-2002; 2002WO-US009107.
 XX AC 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.

PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B, Mansouri K;
 PI Donagai M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansouri K;
 PI McDonald M, Pinder B, Viola C, Wrezel O;
 XX DR WPI; 2003-468119/44.
 XX DR N-PSDB; ADD15501.

XX Novel crystallized recombinant polypeptides from *Staphylococcus aureus*,
 PT *Streptococcus pneumoniae* and *Escherichia coli* and which are involved in
 PT membrane biosynthesis, useful as targets for pathogenic bacteria.
 XX
 CC Claim 86; SEQ ID NO 67; 325pp; English.
 XX
 CC This invention relates to the structural and functional characterisation
 CC of microbial polypeptides from *Staphylococcus aureus* (*S. aureus*),
 CC *Streptococcus pneumoniae* (*S. pneumoniae*) and *Escherichia coli* (*E. coli*)
 CC that provide novel antimicrobial targets. Specifically, it refers to
 CC polypeptides that are involved in membrane biosynthesis, which play a
 CC critical role in the life cycle and viability of their pathogenic species
 CC of origin, and hence provide valuable drug targets. Furthermore, the
 CC invention describes modified version of these proteins that facilitate
 CC fusion proteins. These proteins provide structural and functional
 CC information to aid the discovery of therapeutic molecules to treat
 CC disorders associated with a particular pathogenic species. As such, they
 CC are useful for inducing an immunological response in an individual and as
 CC an antigen for vaccination purposes. The polypeptides are also useful for
 CC developing antimicrobial agents for use as surface disinfectants,
 CC personal hygiene applications and as food preservatives or in treating
 CC food products to eliminate potential pathogens. This polypeptide sequence
 CC is the ACCA protein encoded by experimentally predicted DNA from *E. coli*
 CC invention.
 XX SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 7; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 70 PORPyYL 76

RESULT 37
 ABU40545 DE ABU40545 standard; protein; 320 AA.
 XX AC ABU40545;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #26072.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Proteus sp.
 XX PN WO200277183-A2.
 XX DT 03-OCT-2002.
 XX DE 21-MAR-2002; 2002WO-US009107.
 XX AC 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WI; 2003-029926/02.
 DR N-PSDB; ACA4415.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 68469; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the antisense
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 320 AA;

RESULT 38

Query Match	87.9%	Score	29	DB	6	Length	320
Best Local Similarity	71.4%	Pred. No.	6.9e+02				
Matches	5	Conservative	0	Mismatches	2	Indels	0
Oy	2	PXRPyXL	8				
Db	71	PMRPyTL	77				

XX DE Protein encoded by Prokaryotic essential gene #8693.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX DT 19-JUN-2003 (first entry)

RESULT 39

Query Match	87.9%	Score	29	DB	6	Length	321
Best Local Similarity	71.4%	Pred. No.	6.9e+02				
Matches	5	Conservative	0	Mismatches	2	Indels	0
Oy	2	PXRPyXL	8				
Db	67	PQRPyTL	73				

XX OS *Bordetella pertussis*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX XX

DE Protein encoded by Prokaryotic essential gene #8184.
 XX KW Antisense; prokaryotic gene; cell proliferation; drug design.
 XX OS Burkholderia mallei.
 PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PR 21-MAR-2002; 2002WO-US09107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094893.
 PR 23-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI; 2003-022926/02.
 XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 50581; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 the 6213 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-required gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism's activity; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene
 product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 strains; or (13) identifying the target of a compound that inhibits the
 proliferation of an organism. The antisense nucleic acids are useful for
 identifying proteins or screening for homologous nucleic acids required
 for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 required for proliferation in cells other than S. aureus, S. typhimurium,
 K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 the target prokaryotic essential genes. Note: The sequence data for this
 sequence did not form part of the printed specification, but was obtained
 in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 SQ Sequence 323 AA;

Query Match Score 29; DB 6; Length 323;
 Best Local Similarity 71.4%; Pred. No. 6.9e-02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; N mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPXL 8
 Db 67 PORPYTL 73

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XX
SQ Sequence 323 AA;

Query Match 87.9%; Score 29; DB 6; Length 323;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
| || |
67 PQRPYTL 73

Search completed: March 28, 2005, 08:35:06
Job time : 72 secs

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